

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 21, 2006, 00:15:36 ; Search time 196 Seconds
(without alignments)
41.989 Million cell updates/sec

Title: US-09-857-000a-11

Perfect score: 91

Sequence: 1 RGRLSYRRRFTSTGR 18

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_8.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	100.0	18	2	AAW99412
2	91	100.0	18	3	AAW93615
3	91	100.0	18	3	AAW93179
4	91	100.0	18	3	AAW93177
5	91	100.0	18	5	AAW48469
6	91	100.0	18	6	AAW43980
7	91	100.0	18	6	ABR94452
8	91	100.0	18	6	ABR70228
9	91	100.0	18	7	AAE38690
10	91	100.0	18	7	ADC42901
11	91	100.0	18	7	ADCS1568
12	91	100.0	18	7	ADG28016
13	91	100.0	18	7	ADL88652
14	91	100.0	18	8	ADG73831
15	91	100.0	18	8	ADH58869
16	91	100.0	18	8	ADH89792
17	91	100.0	18	8	ADN03484
18	91	100.0	18	8	ADR88701
19	91	100.0	18	9	ADU15732
20	91	100.0	18	9	ABEB28493
21	91	100.0	19	7	ADES1567
22	91	100.0	19	8	ADR88700
23	81	89.0	18	2	AAW99403

24	81	89.0	18	3	AAW93616
25	81	89.0	18	6	ABR43977
26	81	89.0	18	8	ADN03481
27	80	87.9	18	6	AAE29879
28	79	86.8	18	5	AAW48494
29	73	80.2	18	5	AAW48495
30	73	80.2	18	8	ADH59545
31	69	75.8	18	5	AAW48475
32	67	73.6	18	8	AAW18153
33	67	73.6	18	8	ADL18453
34	66	72.5	18	2	AAW22007
35	66	72.5	18	2	AAW22005
36	65	71.4	18	2	AAW36429
37	65	71.4	18	2	AAW09085
38	65	71.4	18	2	AAW09084
39	65	71.4	18	8	ADL18459
40	65	71.4	18	8	ADL18460
41	65	71.4	18	8	ADL18471
42	64	70.3	18	2	AAW18151
43	64	70.3	18	2	AAW18152
44	64	70.3	18	8	ADL18451
45	64	70.3	18	8	ADL18452
46	63	69.2	18	2	AAW18150
47	63	69.2	18	8	ADL18466
48	63	69.2	18	8	ADL18450
49	63	69.2	18	8	ADL18461
50	62	68.1	18	8	ADL18467
51	62	68.1	18	8	ADL18462
52	61	67.0	18	2	AAW78751
53	61	67.0	18	2	AAW78776
54	61	67.0	18	2	AAW36353
55	61	67.0	18	2	AAW36322
56	61	67.0	18	2	AAW36208
57	61	67.0	18	2	AAW35578
58	61	67.0	18	2	AAW09073
59	61	67.0	18	2	AAW18144
60	61	67.0	18	2	AAW18130
61	61	67.0	18	2	AAW29556
62	61	67.0	18	2	AAW66458
63	61	67.0	18	2	AAW22018
64	61	67.0	18	3	AAW93608
65	61	67.0	18	3	AAW91757
66	61	67.0	18	3	AAW81680
67	61	67.0	18	3	AAW93170
68	61	67.0	18	4	AAW91843
69	61	67.0	18	4	AAW35050
70	61	67.0	18	6	ABU59635
71	61	67.0	18	6	ABR84445
72	61	67.0	18	6	ABP72292
73	61	67.0	18	7	ADH58554
74	61	67.0	18	7	ADK11582
75	61	67.0	18	7	ADK11582
76	61	67.0	18	8	ADD35354
77	61	67.0	18	8	ADD67921
78	61	67.0	18	8	ADL18414
79	61	67.0	18	8	ADL18442
80	61	67.0	18	8	ADL18379
81	61	67.0	18	8	ADL18396
82	61	67.0	18	8	ADL18428
83	61	67.0	18	8	ADQ35258
84	61	67.0	18	8	ADQ15519
85	61	67.0	18	9	ADY67506
86	61	67.0	18	9	ABE21993
87	61	67.0	18	10	ABE99050
88	61	67.0	19	5	AAU090981
89	61	67.0	19	9	ADX08359
90	61	67.0	23	8	ADL18373
91	61	67.0	23	8	AAW25081
92	61	67.0	149	2	AAW09087
93	61	67.0	149	2	ADL18362
94	60	65.9	18	2	AAW78773
95	60	65.9	18	2	AAW78765
96	60	65.9	18	2	AAW18148

AAW93616	Peptide w
ABR43977	Beta-stra
ADN03481	Beta-stra
AAE29879	Membrane
AAW48494	Antibioti
AAW48495	Antibioti
ADH59545	SynB6 pep
AAW48475	Antibioti
AAW18153	Cationic,
ADL18453	Antimicro
AAW22007	Antimicro
AAW22005	Antimicro
AAW36429	Antimicro
AAW09085	Cationic,
AAW09084	Cationic,
ADL18459	Antimicro
ADL18460	Antimicro
ADL18471	Antimicro
AAW18151	Cationic,
AAW18152	Cationic,
ADL18451	Antimicro
ADL18452	Antimicro
AAW18150	Cationic,
ADL18466	Antimicro
ADL18450	Antimicro
ADL18461	Antimicro
ADL18467	Antimicro
ADL18462	Antimicro
AAW78751	Protegrin
AAW78776	Protegrin
AAW36353	Antimicro
AAW36322	Antimicro
AAW36208	Antimicro
AAW35578	Antimicro
AAW09073	Cationic,
AAW18144	Cationic,
AAW18130	Cationic,
AAW29556	Porcine p
AAW66458	Cationic
AAW22018	Protegrin
AAW93608	Protegrin
AAW91757	Cationic
AAW81680	Protegrin
AAW93170	Protegrin
AAW91843	Antimicro
AAW35050	Porcine p
ABU59635	Cationic
ABR84445	Protegrin
ABP72292	Antimicro
ADH58554	Amphiphil
ADK11582	Taxoid ca
ADD35354	Antimicro
ADD67921	Protegrin
ADL18414	Antimicro
ADL18442	Antimicro
ADL18379	Pig antim
ADL18396	Antimicro
ADL18428	Antimicro
ADQ35258	Rhesus th
ADQ15519	Antimicro
ADY67506	Tumor cel
ABE21993	Protegrin
ABE99050	Tumor tis
AAU090981	Transplan
ADX08359	Protegrin
ADL18373	Pig prote
AAW25081	Antimicro
AAW09087	Antimicro
ADL18362	Pig prote
AAW78773	Protegrin
AAW78765	Protegrin
AAW18148	Cationic,

97 60 65.9 18 2 AAW18149 Aaw18149 Cationic,
 98 60 65.9 18 2 AAW18147 Aaw18147 Cationic,
 99 60 65.9 18 8 ADL18447 Adl18447 Antimicro
 100 60 65.9 18 8 ADL18439 Adl18439 Antimicro

ALIGNMENTS

RESULT 1
 AAW99412
 ID AAW99412 standard; peptide; 18 AA.
 AC AAW99412;
 XX
 DT 08-JUN-1999 (first entry)
 XX
 DE Protegrin derivative peptide SM2196.
 XX
 KW Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure;
 KW disulphide bridge; antibody; ribozyme; antitumour agent; antiviral;
 KW anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;
 KW nucleus; blood-brain barrier.
 XX
 OS Synthetic.
 XX
 PN WO9907728-A2.
 XX
 PD 18-FEB-1999.
 XX
 PF 06-AUG-1998; 98WO-FR001757.
 XX
 PR 12-AUG-1997; 97FR-00010297.
 XX
 PA (SYNT-) SYNT:EM SA.
 XX
 PI Calas B, Grassy G, Chavanieu A, Kaczorek M;
 XX
 DR WPI; 1999-190034/16.
 XX
 PT Derivatives of antibiotic peptides lacking disulfide bridges - used as
 PT carriers to deliver active agents into cells.
 XX
 PS Claim 7; Page 28; 37pp; French.
 XX
 CC This peptide represents a linear derivative of the protegrin family of
 CC peptide antibiotics. Protegrin antibiotics form part of the peptide
 CC antibiotic family which contain a beta-sheet secondary structure linked
 CC by disulphide bridges. The new derivatives are linear and lack the
 CC disulphide bridge. The novel derivatives are used to deliver active
 CC agents to an organism, e.g. therapeutic proteins, antibodies (or their
 CC fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents,
 CC antivirals and anti-inflammatories, etc. The derivatives are non-toxic
 CC and non-lytic but can cross mammalian cell membranes rapidly by a passive
 CC mechanism, so can deliver active agents to cytoplasm and nucleus,
 CC including crossing the blood-brain barrier
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFRSTGTGR 18
 |||||
 Db 1 RGGRLSYRRRFRSTGTGR 18

RESULT 2
 AAY93615
 ID AAY93615 standard; peptide; 18 AA.
 XX
 AC AAY93615;

XX 25-SEP-2000 (first entry)
 DT Peptide which may be linked to anticancer agents.
 XX
 DE Anticancer agent; cancer cell; resistance; P-glycoprotein pump; cancer.
 XX
 OS Unidentified.
 XX
 PN WO200032237-A1.
 XX
 PD 08-JUN-2000.
 XX
 PF 26-NOV-1999; 99WO-FR002939.
 XX
 PR 30-NOV-1998; 98FR-00015073.
 XX
 PA (SYNT-) SYNT:EM SA.
 XX
 PI Tamsamani J, Kaczorek M, Colin De Verdier A;
 XX
 DR WPI; 2000-412166/35.
 XX
 PT New composition useful for cancer treatment and prevention, contains
 PT anticancer agent and peptide vector that transports agent into cells.
 XX
 PS Disclosure; Page 8; 34pp; French.
 XX
 CC The specification describes a pharmaceutical composition, which comprises
 CC at least one anticancer agent associated with at least one peptide that
 CC can transport it into cancer cells and which inhibits development of
 CC resistance to the anticancer agent. By using the peptide as a vector for
 CC delivery of the anticancer agent, mechanisms that cause cancer cells to
 CC become resistant to the agent, particularly the P-glycoprotein pump, are
 CC avoided. Also, peptides are easily produced by chemical synthesis, can be
 CC coupled easily to the agent, cross mammalian cell membranes rapidly by a
 CC passive mechanism (no receptors required), and are non-toxic and non-
 CC lytic. The compositions are used to treat cancer. The present sequence
 CC represents a peptide which may be linked to the anticancer agents of the
 CC invention
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFRSTGTGR 18
 |||||
 Db 1 RGGRLSYRRRFRSTGTGR 18

RESULT 3
 AAY93179
 ID AAY93179 standard; peptide; 18 AA.
 XX
 AC AAY93179;

XX 06-DEC-2000 (first entry)
 DT Protegrin-like peptide antibiotic Dal-SynB1.
 XX
 DE Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial;
 KW blood-brain barrier; diagnostic; central nervous system; protegrin;
 KW Antenapedia; tachyplesin; peptide antibiotic; Alzheimer's disease;
 KW cancer; Parkinson's disease; depression; pain; meningitis; dalargin.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Cross-links 1
 FT /note= "cross-links to a molecule of dalargin via a
 FT disulphide linker"

XX WO200032236-A1.
 XX 08-JUN-2000.
 XX 26-NOV-1999; 99WO-FR002938.
 XX 30-NOV-1998; 98FR-00015074.
 XX (SYNT-) SYNT:EM SA.
 XX
 XX Clair P, Kaczorek M, Tamsamani J;
 XX WPI; 2000-422871/36.
 XX
 XX Use of linear peptides as vectors for active ingredients, useful for
 XX diagnosis and treatment of central nervous system diseases, can transport
 XX agents passively across the blood-brain barrier.
 XX
 XX Example II; Page 20; 54pp; French.
 XX
 XX The invention relates to the use of linear peptides, coupled to an active
 XX agent, to prepare a composition able to cross the blood-brain barrier
 XX for diagnosis or treatment of disorders localised in the central nervous
 XX system. The linear peptide preferably has the formula: (a) X1- X16; (b);
 XX BXXBXXBXXBXXBXXB; or (c) BXXBXXBXXBXXBXXB, where: each of X1-X16 are
 XX amino acids (aa), of which 6-10 of them are hydrophobic and X6 must be
 XX Trp; each B is aa containing a side chain that includes a basic group;
 XX and each X is an aliphatic or aromatic aa. The linear peptide may be
 XX retro forms of (a)-(c) containing D- and/or L-form aa, or a fragment
 XX containing at least 5, preferably at least 7 consecutive aa from (a)-(c).
 XX Peptides able to cross the BBB include protegrins, Antennapedia,
 XX tachypleins, transportin, etc. Of these several families have cytolytic
 XX effects and are termed peptide antibiotics. They fall into 3 main
 XX categories based on their structure: (i) peptides with alpha-helices,
 XX e.g. cecropins and maganins; (ii) peptides with disulphide bond-linked
 XX beta-sheets, e.g. protegrin, tachypleins, defensins; (iii) peptides with
 XX no major structure but containing bends due to the presence of Pro
 XX residues, e.g. bactericins and PR39. The peptides of the invention fall
 XX into the peptide antibiotic categories defined above: (a)-peptides are
 XX based on the Antennapedia family peptides; (b)-peptides are based on
 XX protegrins; and (c)-peptides are based on tachypleins. This sequence
 XX represents a synthetic linear peptide designed on peptides able to cross
 XX the BBB and is conjugated to a daltargin molecule by a disulphide linker.
 XX Conjugates of the linear peptides and the active agent are particularly
 XX used to treat, prevent or diagnose brain cancer, Alzheimer's or
 XX Parkinson's diseases, depression, pain and meningitis, but also for
 XX studying drug behaviour in BBB models
 XX
 XX Sequence 18 AA;
 XX
 XX Query Match 100.0%; Score 91; DB 3; Length 18;
 XX Best Local Similarity 100.0%; Pred. No. 1.8e-07; Indels 0; Gaps 0;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 RGGRLSYRRRFFSTGTGR 18
 XX |||||
 XX Db 1 RGGRLSYRRRFFSTGTGR 18
 XX
 XX RESULT 4
 XX AA93177
 XX ID AA93177 standard; peptide; 18 AA.
 XX
 XX AC AA93177;
 XX
 XX XX 06-DEC-2000 (first entry)
 XX
 XX XX Protegrin-like peptide antibiotic Doxo-SynB1.
 XX
 XX DE
 XX DE Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial;
 XX KW blood-brain barrier; diagnostic; central nervous system; protegrin;
 XX KW Antennapedia; tachyplein; peptide antibiotic; Alzheimer's disease;

KW cancer; Parkinson's disease; depression; pain; meningitis.
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Modified-site 1
 XX /note= "linked to doxorubicin via a succinate (-CO-(CH2)2
 XX -CO-) linker; optionally linked to benzylpenicillin by a
 XX glycoamide linker"
 XX
 XX WO200032236-A1.
 XX 08-JUN-2000.
 XX 26-NOV-1999; 99WO-FR002938.
 XX 30-NOV-1998; 98FR-00015074.
 XX (SYNT-) SYNT:EM SA.
 XX
 XX Clair P, Kaczorek M, Tamsamani J;
 XX WPI; 2000-422871/36.
 XX
 XX Use of linear peptides as vectors for active ingredients, useful for
 XX diagnosis and treatment of central nervous system diseases, can transport
 XX agents passively across the blood-brain barrier.
 XX
 XX Example I; Page 13; 54pp; French.
 XX
 XX The invention relates to the use of linear peptides, coupled to an active
 XX agent, to prepare a composition able to cross the blood-brain barrier
 XX for diagnosis or treatment of disorders localised in the central nervous
 XX system. The linear peptide preferably has the formula: (a) X1- X16; (b);
 XX BXXBXXBXXBXXBXXB; or (c) BXXBXXBXXBXXBXXB, where: each of X1-X16 are
 XX amino acids (aa), of which 6-10 of them are hydrophobic and X6 must be
 XX Trp; each B is aa containing a side chain that includes a basic group;
 XX and each X is an aliphatic or aromatic aa. The linear peptide may be
 XX retro forms of (a)-(c) containing D- and/or L-form aa, or a fragment
 XX containing at least 5, preferably at least 7 consecutive aa from (a)-(c).
 XX Peptides able to cross the BBB include protegrins, Antennapedia,
 XX tachypleins, transportin, etc. Of these several families have cytolytic
 XX effects and are termed peptide antibiotics. They fall into 3 main
 XX categories based on their structure: (i) peptides with alpha-helices,
 XX e.g. cecropins and maganins; (ii) peptides with disulphide bond-linked
 XX beta-sheets, e.g. protegrin, tachypleins, defensins; (iii) peptides with
 XX no major structure but containing bends due to the presence of Pro
 XX residues, e.g. bactericins and PR39. The peptides of the invention fall
 XX into the peptide antibiotic categories defined above: (a)-peptides are
 XX based on the Antennapedia family peptides; (b)-peptides are based on
 XX protegrins; and (c)-peptides are based on tachypleins. This sequence
 XX represents a synthetic linear peptide designed on peptides able to cross
 XX the BBB and is conjugated to a doxorubicin molecule by a succinate
 XX linker. The peptide may also be linked to a benzylpenicillin molecule by
 XX a glycoamide linker. Conjugates of the linear peptides and the active
 XX agent are particularly used to treat, prevent or diagnose brain cancer,
 XX Alzheimer's or Parkinson's diseases, depression, pain and meningitis, but
 XX also for studying drug behaviour in BBB models
 XX
 XX Sequence 18 AA;
 XX
 XX Query Match 100.0%; Score 91; DB 3; Length 18;
 XX Best Local Similarity 100.0%; Pred. No. 1.8e-07; Indels 0; Gaps 0;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 RGGRLSYRRRFFSTGTGR 18
 XX |||||
 XX Db 1 RGGRLSYRRRFFSTGTGR 18
 XX
 XX RESULT 5
 XX AA948469
 XX ID AA948469 standard; peptide; 18 AA.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTGTGR 18
 |||||

Db 1 RGGRLSYRRRFFSTGTGR 18
 |||||

RESULT 8
 ABP70228
 ID ABP70228 standard; peptide; 18 AA.
 XX AC
 XX DT
 XX DT 07-APR-2003 (first entry)
 XX DE
 XX DE Amino acid sequence of membrane translocating peptide SynB1.
 XX KW Lipid-nucleic acid complex; polycation; targeting factor; gene therapy;
 KW cancer; infection; immune deficiency; gene defect; genetic disease;
 KW membrane translocating peptide.
 XX OS Unidentified.
 XX PN WO200288318-A2.
 XX PD 07-NOV-2002.
 XX PF 30-APR-2002; 2002WO-US013609.
 XX PR 30-APR-2001; 2001US-0287786P.
 XX PA (TARG-) TARGETED GENETICS CORP.
 XX PA (EMER-) EMERALD GENE SYSTEMS LTD.
 XX PI Harvie P, Paul R, Cudmore S, O'mahony DJ;
 XX WPI; 2003-183837/18.
 XX PT Lipid-nucleic acid complex useful for delivering a nucleic acid to a
 PT cell, comprises compacted nucleic acid, polycation, targeting factor and
 PT lipid, and does not comprise protamine or its salt.
 XX PS Disclosure; Page 42; 259pp; English.
 XX CC The specification describes a lipid-nucleic acid complex, comprising a
 CC compacted nucleic acid, a polycation, a targeting factor and a lipid, but
 CC not a protamine. The targeting factor increases cellular bioavailability
 CC of the nucleic acid without interaction with a specific outer cell
 CC surface membrane receptor. The mean diameter of the complex is greater
 CC than 100 nm and less than 400 nm. The lipid-nucleic acid complex is
 CC useful for delivering a nucleic acid to a cell in vivo, e.g. for gene
 CC therapy. It reduces levels of inflammatory cytokines such as tumour
 CC necrosis factor-alpha. The complex is useful for manufacturing a
 CC medicament for treating or diagnosing a variety of diseases, conditions
 CC or syndromes such as cancer, bacterial, viral or parasitic infections,
 CC immune deficiencies, gene defects, and gene deficiencies (e.g. inherited
 CC genetic diseases). The present sequence represents a membrane
 CC translocating peptide, which is used as the targeting factor in lipid-
 CC nucleic acid complexes of the invention

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTGTGR 18
 |||||

Db 1 RGGRLSYRRRFFSTGTGR 18
 |||||

RESULT 10
 ADC42901
 ID ADC42901 standard; peptide; 18 AA.
 XX AC
 XX AC ADC42901;
 XX DT 18-DEC-2003 (first entry)
 XX DE
 XX DE Syn B1 from Antennapedia homeodomain protein #SEQ ID 15.
 XX

Db 1 RGGRLSYRRRFFSTGTGR 18

RESULT 9
 AAE38690
 ID AAE38690 standard; peptide; 18 AA.
 XX AC
 XX AC AAE38690;
 XX DT 04-DEC-2003 (first entry)
 XX DE
 XX DE SynB1 peptide.
 XX KW Artificial transcription factor; DNA binding protein; ATF; ZFP; therapy;
 KW zinc finger protein; crop protection; disease-resistant; transgenic;
 KW transgenic plant.
 XX OS Unidentified.
 XX PN WO2003062455-A2.
 XX PD 31-JUL-2003.
 XX PF 23-JAN-2003; 2003WO-US0002358.
 XX PR 23-JAN-2002; 2002US-00057408.
 XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX PI Sera T;
 XX WPI; 2003-646071/61.
 XX PT Preparing an artificial transcription factor (ATF) capable of modulating
 PT expression of a gene by interaction with a target site associated with
 PT the gene, for treating plant disease, comprises preparing a combinatorial
 PT library of ATFs.
 XX PS Disclosure; Page 66; Opp; English.
 XX CC The invention relates to a method of preparing artificial transcription
 CC factor (ATF) capable of modulating expression of a gene by interaction
 CC with a target site associated with the gene. The method comprises
 CC preparing a combinatorial library of ATFs, each of the ATFs comprising a
 CC DNA-binding domain and a transcriptional regulatory domain. The invention
 CC also relates to DNA binding proteins comprising zinc finger domains and
 CC particularly to the identification of a context-independent recognition
 CC code to zinc finger domains. The methods are useful for treating disease
 CC in a plant, for crop protection and for producing genetically transformed
 CC disease-resistant plants. The present sequence is synB1 peptide used to
 CC illustrate the method of the invention

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 7; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTGTGR 18
 |||||

Db 1 RGGRLSYRRRFFSTGTGR 18
 |||||

RESULT 10
 ADC42901
 ID ADC42901 standard; peptide; 18 AA.
 XX AC
 XX AC ADC42901;
 XX DT 18-DEC-2003 (first entry)
 XX DE
 XX DE Syn B1 from Antennapedia homeodomain protein #SEQ ID 15.
 XX

KW Zinc finger protein; ZFP; artificial zinc finger protein; AFP;
 KW nuclear envelope; nuclear lamina; heterochromatin; GCL protein;
 KW gene expression; cytokine; interleukin; oncogene; angiogenesis factor;
 KW drug resistance protein; growth factor; tumour suppressor; DNA binding.
 XX
 OS Synthetic.
 XX
 PN WO2003062447-A2.
 XX
 XX 31-JUL-2003.
 XX
 XX 17-JAN-2003; 2003WO-US001529.
 XX
 XX 18-JAN-2002; 2002US-0350163P.
 PR 23-JAN-2002; 2002US-035115P.
 XX
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA
 XX Sera T;
 XX
 XX WPI; 2003-803624/75.
 DR
 XX
 XX Nucleic acid target-specific chimeric proteins comprising a nuclear-
 PT envelope and/or nuclear lamina binding domain and a DNA binding domain
 PT used in methods to repress or down-regulate expression of selected genes.
 PT
 XX
 XX Disclosure; SEQ ID NO 15; 60pp; English.
 PS
 XX
 CC The invention relates to a nucleic acid target-specific chimeric protein
 CC comprising one or more first domains capable of specifically binding a
 CC nucleotide sequence associated with a target gene, and one or more second
 CC domains capable to associating with the nuclear periphery, where at least
 CC one of the first domains is heterologous with respect to at least one of
 CC the second domains. The one or more first domains comprise at least three
 CC zinc finger proteins (ZFP's) or artificial zinc finger proteins (AZP's)
 CC directly joined to one another. The one or more second domains directly
 CC or indirectly associate with or bind to the nuclear envelope, the nuclear
 CC lamina, heterochromatin or any combinations of these. One of the second
 CC domains is a GCL protein or a binding moiety of a GCL protein. The
 CC chimeric proteins of the invention and the nucleic acids encoding them
 CC can be used to repress, down regulate or decrease gene expression of a
 CC target gene in an eukaryotic organism, including yeast animals and plants
 CC and may encode a cytokine, an interleukin, an oncogene, an angiogenesis
 CC factor, an anti-angiogenesis factor, a drug resistance protein, a growth
 CC factor or a tumour suppressor. The chimeric proteins can be used to
 CC inhibit the expression of a disease-associated gene. The invention
 CC provides a new method of transcriptional repression of genes. Previously
 CC used transcription factors have limited utility or are limited to a set
 CC of closely related target sequences. The zinc finger proteins of the
 CC invention are DNA binding proteins with predetermined sequence
 CC specificity for unique target sequences in a large complex genome. An
 CC example from the invention demonstrates the repression of the human
 CC vascular endothelial growth factor A (VEGF-A) gene. The current sequence
 CC represents Syn B1 from the Antennapedia homeodomain protein. This peptide
 CC is capable of carrying substances across the blood brain barrier.
 XX
 SQ Sequence 18 AA;
 Query Match 100.0%; Score 91; DB 7; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RGGRLSYRRRFFSTGTGR 18
 |||||
 Db 1 RGGRLSYRRRFFSTGTGR 18
 |||||
 RESULT 11
 ADE51568
 ID ADE51568 standard; peptide; 18 AA.
 XX
 AC ADE51568;
 XX

DT 29-JAN-2004 (first entry)
 XX
 DE Peptide #6 to transport cyclosporin compound across blood brain barrier.
 XX
 KW neuroprotective; cerebroprotective; vulnery; hemostatic;
 KW anticoagulant; neuroleptic; thrombolytic; anticoagulant; vasotropic;
 KW nootropic; antiparkinsonian; cytostatic; antidiabetic; antibacterial;
 KW anti-HIV; ophthalmological; antiinflammatory; virucide; protozoacide;
 KW immunosuppressive; dermatological; antithyroid; antidote; antirheumatic;
 KW antiarthritic; antipsoriatic; endocrine-general; cyclophilin inhibitor;
 KW calcineurin inhibitor;
 KW neurotoxic calcium-dependent enzyme cascade blocker;
 KW mitochondrial stabilizer; cyclosporin; transporter; blood-brain barrier.
 XX
 OS Synthetic.
 XX
 PN WO2003070755-A2.
 XX
 XX 28-AUG-2003.
 PD
 XX
 XX 24-FEB-2003; 2003WO-FR000591.
 PF
 XX 22-FEB-2002; 2002FR-00002299.
 PR
 XX (SYNT-) SYNT:EM.
 XX (MAAS-) MAAS BIOLAB LLC.
 PA
 XX Mouchet P, Rees AR, Elmer E, Keep MF;
 PI
 XX WPI; 2003-712609/67.
 DR
 XX
 XX New cyclosporin derivatives, containing bonded peptide vector for
 PT crossing blood-brain barrier, used for treating cerebral disorders such
 PT as neurodegenerative diseases, cerebral trauma or cerebrovascular
 PT accidents.
 PT
 XX Disclosure; SEQ ID NO 6; 77pp; French.
 PS
 XX
 CC The invention relates novel cyclosporin compounds (I) comprise at least
 CC one cyclosporin molecule (II) and at least one peptide vector (III)
 CC capable of transporting (I) across the blood-brain barrier. (I) are used
 CC for the treatment or prevention of: (i) acute neurological disorders,
 CC e.g. due to traumatic cerebral lesions, spinal cord lesions, exposure to
 CC radiation, chemotherapy, epilepsy, schizophrenia, cerebral or spinal
 CC surgery, cerebrovascular accidents, embolic cerebrovascular accident,
 CC global cerebral ischemia, ruptured aneurysms, subarachnoid hemorrhage,
 CC vascular spasms or hemorrhagic vascular accidents; (ii) neurodegenerative
 CC diseases selected from Alzheimer's disease, Parkinson's disease,
 CC Huntington's disease, Down syndrome, Charcot disease, spino-muscular
 CC atrophy, bulbar paralysis, schizophrenia, Tourette syndrome, diffuse
 CC cerebrocortical atrophy, Lewy body dementia, mesolimbocortical dementia,
 CC thalamic degeneration, Pick disease, multisystem dementia, cortico-
 CC striato-spinal degeneration, Shy-Drager syndrome, Richardson-Steale-
 CC Olzewski syndrome, Parkinson-amyotrophic lateral sclerosis-Guam dementia
 CC complex, post-polio syndrome, olivo-cerebellar atrophy, Friedreich
 CC ataxia, paraneoplastic syndrome, traumatic chronic encephalopathy
 CC (boxer's dementia), Wilson disease, Menke disease, Tay-Sachs gangliosidosis,
 CC Krabbe disease, peripheral neuropathy, diabetic neuropathy or aging;
 CC (iii) prion diseases, such as Creutzfeldt Jacob disease (CJD), atypic CJD,
 CC kuru, scrapie or bovine spongiform encephalitis; (iv) retroviral
 CC diseases, e.g. AIDS dementia, AIDS myelopathy; AIDS peripheral neuropathy
 CC or tropical paraparesis; (v) visual and retinal disorders, e.g. glaucoma-
 CC related degeneration, macular degeneration, diabetic degeneration,
 CC diabetic retinopathy, degeneration-related inflammation, detached retina,
 CC optical neuritis, optic nerve lesions, optical chiasm or optical tractus
 CC and retinal lesions caused by photons, trauma, ischemia or elevated
 CC intracranial pressure; (vi) viral and bacterial diseases associated with
 CC encephalopathy, including herpetic, equine, post-vaccination, Japanese or
 CC Nile encephalitis, meningitis, rabies, poliomyelitis, progressive
 CC multifocal leuko-encephalopathy, subacute sclerotic panencephalitis,
 CC cerebral malaria, Lyme disease or neurosyphilis; (vii) immunological
 CC diseases, e.g. plaque sclerosis, Guillain-Barre syndrome, lupus
 CC erythematosus or Graves disease; (viii) the effects of neurotoxins,

CC including aminoglycosides, chlorinated hydrocarbons, organophosphates,
 CC insecticides, herbicides, paraquat, nerve gas, 1-methyl-4-phenyl-1,2,3,6-
 CC tetrahydropyridine, rotenone, cyanide, carbon monoxide, methanol,
 CC ethanol, mercury, arsenic, chemotherapeutic agents (e.g. methotrexate,
 CC mercaptopurine, fluorouracil, nitrosoureas, hydroxyurea, cisplatin,
 CC carboplatin, daunorubicin, etoposide, vincristine, vinblastine, taxol (or
 CC derivatives) or cyclophosphamide) or corticosteroids; (ix) metabolic
 CC encephalopathy, e.g. hepatic or uremic encephalopathy; (x) conditions
 CC requiring induction of a non-immune state, e.g. transplantation of
 CC organs, tissues or cells or immune or autoimmune diseases such as
 CC rheumatoid arthritis, eczema, psoriasis or alopecia; or (xi)
 CC chemotherapy-resistant tumors. This sequence is an example of the peptide
 CC part of the compound.
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 7; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18
 |||||
 DB 1 RGGRLSYRRRFFSTGTGR 18

RESULT 12
 ADG28016
 ID ADG28016 standard; peptide; 18 AA.
 AC ADG28016;
 XX
 DT 26-FEB-2004 (first entry)
 DE Protegrin/porcine leukocyte SynB1 membrane fusion sequence.
 XX
 KW fusion protein; cold shock domain; membrane translocation sequence; CspA;
 KW CspB; CspC; CspD; rpi S1 binding domain; eukaryotic Y-box protein;
 KW DNA binding protein B; DBPB; DBPA; EFE-1; MRNP3; MRNP4; FRG Y1;
 KW nuclease-sensitive element binding protein 1; NSE1;
 KW DNA condensation domain; DNA binding domain; SPKR;
 KW nuclear localisation sequence; NLS; protein purification tagged sequence;
 KW gene delivery; protegrin; porcine leukocyte; synB1;
 KW membrane fusion sequence.
 XX
 OS Synthetic.
 XX
 PN US2003211590-A1.
 XX
 PD 13-NOV-2003.
 XX
 PF 13-MAY-2002; 2002US-00144549.
 XX
 PR 13-MAY-2002; 2002US-00144549.
 XX
 PA (HWUP/) HWU P L.
 XX
 PI HWU PL;
 XX
 XX WPI; 2003-901590/82.
 XX

PT New fusion protein comprising a cold shock domain, and a membrane
 PT translocation sequence, useful for delivering DNAs and RNAs to in vivo
 PT cells for gene delivery.

XX Claim 9; SEQ ID NO 17; 24pp; English.

XX The invention describes a fusion protein for delivery of a desired
 CC molecule into cells or nuclei, comprising a cold shock domain, its
 CC homologue and functional derivative, and a membrane translocation
 CC sequence or its functional equivalent peptides and/or derivatives. The
 CC fusion protein comprises a cold shock domain that is selected from CspA,
 CC CspB, CspC, CspD, rpi S1 binding domain, eukaryotic Y-box proteins, DNA
 CC binding protein B (DBPB), DBPA, EFE-1, MRNP3, MRNP4, FRG Y1 and nuclease-

CC sensitive element binding protein 1 (NSEP 1). The functional equivalent
 CC derivative of cold shock protein is modified by inserting into the cold
 CC shock domain with a DNA condensation domain or a DNA binding domain. The
 CC DNA condensation or binding domain is selected from DNA condensation
 CC domain (SPKR) 3-4 and the positive charge nuclear localisation sequences
 CC (NLS+). The membrane transduction sequence is protein transduction domain
 CC (PTD) or membrane fusion sequence. The fusion protein further comprises a
 CC protein purification tagged sequence selected from HA, GST, and His6 tag.
 CC The fusion protein is useful for delivering DNAs and RNAs to in vivo
 CC cells for gene delivery, or for delivering nucleic acids to an embryo or
 CC to a living animal for the production of transgenic animal. This is the
 CC amino acid sequence of protegrin/porcine leukocyte derived synB1 membrane
 CC fusion sequence.
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 7; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18
 |||||
 DB 1 RGGRLSYRRRFFSTGTGR 18

RESULT 13
 ADL88652
 ID ADL88652 standard; peptide; 18 AA.
 AC ADL88652;
 XX
 DT 20-MAY-2004 (first entry)
 DE SynB1 membrane fusion sequence peptide.
 XX
 KW fusion protein; cold shock domain; membrane translocation; gene therapy;
 KW transgenic; membrane fusion; SynB1.
 XX
 OS Unidentified.
 XX
 PN JP2004035409-A.
 XX
 PD 05-FEB-2004.
 XX
 PF 15-MAY-2002; 2002JP-00140441.
 XX
 PR 13-MAY-2002; 2002US-00144549.
 XX
 PA (GENE-) GENESHUTTLE BIOPHARM INC.
 XX
 PI HWU PL;
 XX
 XX WPI; 2003-901590/82.
 XX

PT New fusion protein comprising a cold shock domain, and a membrane
 PT translocation sequence, useful for delivering DNAs and RNAs to in vivo
 PT cells for gene delivery.

XX Claim 9; SEQ ID NO 15; 53pp; Japanese.

XX The invention relates to a novel fusion protein for delivery of a desired
 CC molecule into cells or nuclei comprising a cold shock domain, its
 CC homologue and functional derivative and a membrane translocation sequence
 CC or its functionally equivalent peptides and/or derivatives. The fusion
 CC protein of the invention may be useful for delivering DNAs and RNAs to in
 CC vivo cells for gene therapy or for delivering nucleic acids to an embryo
 CC or to a living animal for the production of transgenic animals. The
 CC current sequence is that of a membrane fusion sequence peptide of the
 CC invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 91; DB 7; Length 18;

```
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTSTGR 18
Db 1 RGGRLSYRRRFFSTSTGR 18

RESULT 14
ADG73831
ID ADG73831 standard; peptide; 18 AA.
XX AC
XX ADG73831;
XX 11-MAR-2004 (first entry)
XX Membrane-penetrating peptide SynB1.
DE SynB1; drug delivery; nanoparticle.
XX Unidentified.
XX EP1362599-A2.
PN 19-NOV-2003.
XX 28-JUN-2002; 2002EP-00254597.
XX 17-MAY-2002; 2002KR-00027328.
XX (PACI-) PACIFIC CORP.
XX Chang IS, Park JY, Nam YS, Han SH;
PI WPI; 2004-055143/06.
XX Conjugate of biodegradable aliphatic polyester-based polymer with Tat (49-
PT 57) peptide or peptide chain containing the Tat (49-57) peptide, useful
PT for manufacturing nanoparticle with enhanced intracellular permeability.
XX Disclosure; SEQ ID NO 3; 18pp; English.
XX The present sequence is that of SynB1, a membrane-permeable peptide of
CC protegrins. The peptide has been examined previously as a means for
CC improving drug delivery through the blood-brain barrier. The present
CC invention provides a conjugate of a biodegradable aliphatic polyester-
CC based polymer and the membrane-permeable Tat49-57 peptide ADG73829 from
CC HIV-1, or a peptide including Tat49-57. The Tat49-57 peptide (A) and the
CC biodegradable aliphatic polyester-based polymer (B) are constituted as A-
CC B type or A-B-A type. The conjugate is used to manufacture nanoparticles
CC of average diameter not more than 1,000 nm. These nanoparticles can be
CC used as a drug delivery system with an improved bioavailability in vivo.
XX Sequence 18 AA;

Query Match 100.0%; Score 91; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTSTGR 18
Db 1 RGGRLSYRRRFFSTSTGR 18

RESULT 15
ADH58869
ID ADH58869 standard; peptide; 18 AA.
XX AC
XX ADH58869;
XX 25-MAR-2004 (first entry)
XX Membrane-permeable doxorubicin anticancer agent peptide.
DE
```

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XX conjugate; biodegradable aliphatic polyester-based polymer; Tat (49-57);
KW nanoparticle; intracellular permeability; doxorubicin.
XX Unidentified.
XX US2003220474-A1.
XX 27-NOV-2003.
PD 28-JUN-2002; 2002US-00185593.
XX 28-JUN-2002; 2002US-00185593.
XX (PACI-) PACIFIC CORP.
XX Park JY, Nam YS, Han SH, Chang IS;
PI WPI; 2004-089301/09.
XX Conjugate of biodegradable aliphatic polyester-based polymer with Tat (49-
PT 57) peptide or peptide chain containing the Tat (49-57) peptide, useful
PT for manufacturing nanoparticle with enhanced intracellular permeability.
XX Disclosure; SEQ ID NO 3; 16pp; English.
XX The invention relates to a novel conjugate of a biodegradable aliphatic
CC polyester-based polymer with a Tat (49-57) peptide or a peptide chain
CC containing the Tat (49-57) peptide. The invention further relates to a
CC nanoparticle manufactured using the conjugate. The novel conjugate is
CC useful for manufacturing a nanoparticle with an average diameter of not
CC more than 1000 nm. The conjugate enhances the intracellular permeability
CC of the manufactured nanoparticle. This sequence represents a membrane-
CC permeable doxorubicin anticancer agent peptide of the invention.
XX Sequence 18 AA;

Query Match 100.0%; Score 91; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTSTGR 18
Db 1 RGGRLSYRRRFFSTSTGR 18

RESULT 16
ADH89792
ID ADH89792 standard; peptide; 18 AA.
XX AC
XX ADH89792;
XX 22-APR-2004 (first entry)
XX Cell penetrating peptide (CPP) identification method-related peptide 106.
DE cell-penetrating peptide; CPP; bulk property value Z-E; Z-E1; Z-E2; Z-E3;
XX Z-E4; Z-E5; antidiabetic; neuroprotective; nootropic; antiparkinsonian;
KW cardiant; cytostatic; tranquiliser; immunosuppressive; antidepressant;
KW anticonvulsant; antiinflammatory; analgesic; neuroleptic;
KW ophthalmological; antiulcer; cell-penetration; infectious disease;
KW diabetes type I; diabetes type II; Alzheimer's disease;
KW Parkinson's disease; cancer; prion disease; cardiovascular disease;
KW signal transduction.
XX Unidentified.
XX WO2003106491-A2.
XX 24-DEC-2003.
XX 18-JUN-2003; 2003WO-IB003163.
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PR 18-JUN-2002; 2002SE-00001863.
PR 25-JUN-2002; 2002US-0391788P.
XX (CEPE-) CEPEP AB.
XX
XX Haellbrink M, Pooga M, Metsis M, Kogerman P, Valkna A, Meikas A;
XX Lindgren M, Graeslund A, Eriksson G, Oestensson CG, Budhina M;
XX Zorko M, Elmquist A, Soomets U, Lundberg P, Jaerver P, Saar K;
XX El-Andalousi S, Kilk K, Langel U;
XX WPI; 2004-090832/09.
XX
XX Predicting, designing, detecting, and/or verifying novel cell-penetrating
XX peptide based on assessment of bulk property value of sequences of cell-
XX penetrating peptide.
XX
XX Example 11; Page 17; 148pp; English.
XX
XX This invention relates to a novel method of identifying, designing,
XX detecting, and/or verifying novel cell-penetrating peptide (CPP) based on
XX assessment of bulk property value Z-B of sequences of CPP comprising 5 or
XX more individual average interval values Z-E1, Z-E2, Z-E3, Z-E4 and Z-E5,
XX where Z-E1, Z-E2, Z-E3, Z-E4 and Z-E5 are average values of the
XX respective descriptor values for the residues in the amino acid sequence.
XX The invention may be useful for the development of compounds with an
XX antidiabetic, neuroprotective, nootropic, antiparkinsonian, cardiant,
XX cyostatic, tranquiliser, immunosuppressive, antidepressant,
XX anticonvulsant, antiinflammatory, analgesic, neuroleptic,
XX ophthalmological or anticancer activity as a stimulator of cell-
XX penetration. The method of the invention is useful for identifying a cell-
XX penetrating peptide or protein and/or a cell-penetrating fragment of a
XX peptide or protein. In addition, the invention may be useful for checking
XX cellular penetration properties of a peptide, for producing a cell-
XX penetrating and functional protein-mimicking peptide and for de novo
XX design and production of an artificial cell-penetrating and/or and
XX artificial cell-penetrating and functional protein-mimicking peptide.
XX Compositions developed within the scope of the present invention may be
XX useful for treating infectious diseases, diabetes type I, diabetes type
XX II, Alzheimer's disease, Parkinson's diseases, cancer, prion disease,
XX cardiovascular disease or disorders resulting from perturbed signal
XX transduction. The method of the invention is fast, efficient and reliable
XX for identifying, detecting, designing CPPs and for screening cellular
XX uptake of a broad variety of CPPs in vitro and in vivo. The present
XX sequence is that of a peptide which was used in the exemplification of
XX the invention.
XX
XX SQ Sequence 18 AA;
XX
XX Query Match 100.0%; Score 91; DB 8; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 RGGRLSYRRRRFSTGTGR 18
XX Db 1 RGGRLSYRRRRFSTGTGR 18
XX
XX RESULT 17
XX ADN03484
XX ID ADN03484 standard; peptide; 18 AA.
XX
XX AC ADN03484;
XX
XX 01-JUL-2004 (first entry)
XX
XX Beta-stranded protegrin peptide linear deriative #7.
XX
XX Beta-stranded antibiotic peptide; immune response; therapy; vaccine;
XX protegrin.
XX
XX Unidentified.
XX
XX US2004072340-A1.
XX
XX
XX 15-APR-2004.
XX
XX 15-OCT-2002; 2002US-00270010.
XX
XX 15-OCT-2002; 2002US-00270010.
XX
XX (JOHN/) JOHNSON M E.
XX (DAYF/) HAMILTON DAY F.
XX (KACZ/) KACZOREK M.
XX (TEMS/) TEMSAMANI J.
XX
XX Johnson ME, Hamilton Day F, Kaczorek M, Tamsamani J;
XX WPI; 2004-328576/30.
XX
XX New conjugates of an antigen coupled to a linear derivative of a beta-
XX stranded antibiotic peptide, useful for enhancing the immune response of
XX a mammal to an antigen.
XX
XX Claim 7; SEQ ID NO 10; 21pp; English.
XX
XX The present invention relates to conjugates of an antigen coupled to a
XX linear derivative of a beta-stranded antibiotic peptide. The invention is
XX useful for enhancing the immune response of a mammal to an antigen. The
XX invention is also useful in the production of vaccines. The present
XX sequence is a beta-stranded protegrin (antibiotic) peptide linear
XX derivative.
XX
XX SQ Sequence 18 AA;
XX
XX Query Match 100.0%; Score 91; DB 8; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 RGGRLSYRRRRFSTGTGR 18
XX Db 1 RGGRLSYRRRRFSTGTGR 18
XX
XX RESULT 18
XX ADR88701
XX ID ADR88701 standard; peptide; 18 AA.
XX
XX AC ADR88701;
XX
XX 18-NOV-2004 (first entry)
XX
XX Amino acid sequence of a peptide designated SynB1.
XX
XX disease treatment; active substance transport; bioavailability; SynB1;
XX cyclosporin A.
XX
XX Unidentified.
XX
XX FR2851471-A1.
XX
XX 27-AUG-2004.
XX
XX 24-FEB-2003; 2003FR-00002242.
XX
XX 24-FEB-2003; 2003FR-00002242.
XX
XX (SYNT-) SYNT:EM SA.
XX
XX Rees AR, Mouchet P;
XX WPI; 2004-627939/61.
XX
XX Compound comprising active agent coupled to vector through a linker,
XX useful in human or veterinary medicine, where the linker includes a
XX hydroxyproline residue.
XX
```

PS Disclosure; SEQ ID NO 6; 65pp; French.

XX The specification describes a compound comprising at least one active

CC substance and at least one vector, connected by a linker that includes a

CC hydroxyproline residue. The linker is of a formula given in the

CC specification. The vector modifies the physicochemical or pharmacokinetic

CC properties of the active substance. The active substance is a protein,

CC (poly)peptide, antibody (or fragment), nucleic acid, oligonucleotide,

CC ribozyme, or a chemical for treatment or prevention of human or animal

CC disease, e.g. an antitumour or antiviral agent. Alternatively, it is a

CC radioactive or coloured material, or some other substance suitable as

CC indicator of metabolism or disease. Compounds of the invention are used

CC for treatment, prevention and diagnosis of disease in human or veterinary

CC medicine. They facilitate transport of the active substance across

CC biological barriers and its penetration into cells, and they also modify

CC the bioavailability or solubility of active substances. The present

CC sequence represents a peptide designated SynBl. SynBl was joined to

CC cyclosporin A via a linker to produce exemplary compounds of the

CC invention.

XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.8e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18

DB 1 RGGRLSYRRRFFSTGTGR 18

RESULT 19

ADU15732

ID ADU15732 standard; peptide; 18 AA.

XX

AC ADU15732;

XX

DT 13-JAN-2005 (first entry)

XX

DE MUC1-PDZ domain binding inhibitor transmembrane transporter peptide #20.

XX

KW cytoplasmic domain; MUC1; PDZ domain; transmembrane transporter.

XX

OS Unidentified.

XX

PN WO2004092339-A2.

XX

PD 28-OCT-2004.

XX

PF 12-APR-2004; 2004WO-US011195.

XX

PR 11-APR-2003; 2003US-0462111P.

XX

PR 02-MAY-2003; 2003US-0467728P.

XX

PR 04-JUN-2003; 2003US-0475595P.

XX

PR 11-SEP-2003; 2003US-0502111P.

XX

PR 21-NOV-2003; 2003US-0524188P.

XX

PA (ILEX-) ILEX PROD INC.

PA (ARBO-) ARBOR VITA CORP.

PA (DAND) DANA FARBER CANCER INST.

XX

PI Belmares MP, Lu PS, Garman JD, Jecminek AA, Kharbanda S, Agata N;

PI Kufe DW;

XX

XX WPI; 2004-766852/75.

XX

XX Inhibiting the binding of the cytoplasmic domain of MUC1 to a PDZ domain,

XX comprises contacting the PDZ domain with an agent that competes with the

XX binding of the C-terminal region of the cytoplasmic domain of MUC1 with

XX the PDZ domain.

XX

PS Claim 9; SEQ ID NO 116; 141pp; English.

XX

CC The invention relates to a method of inhibiting the binding of the

CC cytoplasmic domain of MUC1 to a PDZ domain, by contacting the PDZ domain

CC with an effective amount of an agent that competes with the binding of

CC the C-terminal region of the cytoplasmic domain of MUC1 with the PDZ

CC domain. The PDZ domain is ZO-1 d2, SIP1 d1, LIM MYSTIQUE, AIPC, KIAA0751,

CC MAST2, PRIL-16 d1, GRIP2 d5, SITAC 18, NSP or KIAA1526 d1. The agent that

CC competes with binding of the C-terminal region of cytoplasmic domain of

CC MUC1 with the PDZ domain is a peptide of the formula (I): X1-aa2-aal-aa0,

CC where aa0 is a hydrophobic aliphatic amino acid residue or a hydrophobic

CC aromatic amino acid residue; aa2 is a hydrophobic aliphatic amino acid

CC residue, hydrophobic aromatic amino acid residue, polar amino acid

CC residue, basic amino acid residue or an acidic amino acid residue; aal is

CC any amino acid residue; and X1 is a sequence of 0-50 amino acid residues.

CC Preferably aa2-aal-aa0 is selected from SEQ ID NO: 1-40 (ADU15617-

CC ADU15656) and X1 may be selected from SEQ ID NO: 41-94 (ADU15657-

CC ADU15710). The method is useful for inhibiting the binding of the

CC cytoplasmic domain of MUC1 to a PDZ domain. The amino terminal of the X1

CC peptide may also contain a transmembrane transporter peptide. The

CC transporter sequence may be selected from SEQ ID NO: 97-127 (ADU15713-

CC ADU15743). This peptide is derived from a pegelin protein.

XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.8e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18

DB 1 RGGRLSYRRRFFSTGTGR 18

RESULT 20

AE28493

ID AEB28493 standard; peptide; 18 AA.

XX

AC AEB28493;

XX

DT 22-SEP-2005 (first entry)

XX

DE SynBl transduction peptide.

XX

KW Pharmaceutical; nucleic acid delivery; transportan.

XX

OS Synthetic.

XX

PN US2005153913-A1.

XX

PD 14-JUL-2005.

XX

PF 28-JUN-2004; 2004US-00878175.

XX

PR 10-APR-2001; 2001US-00829551.

XX

PA (KOSA/) KOSAK K M.

XX

PI Kosak KM;

XX

DR WPI; 2005-496857/50.

XX

XX Pharmaceutical nucleic acid carrier composition useful in therapeutic

XX applications for targeting delivery of nucleic acids to their site of

XX action, having carrier substance covalently/non-covalently coupled to

XX nucleic acid intercalator.

XX

PS Disclosure; SEQ ID NO 36; 38pp; English.

XX

XX The invention relates to a pharmaceutical nucleic acid carrier

XX composition (C1), comprising a carrier substance covalently or non-

XX covalently coupled to a nucleic acid intercalator, where the nucleic acid

XX intercalator is coupled to a nucleic acid. C1 can be synthesized by

XX coupling a carrier substance to intercalator to produce a carrier

XX substance having intercalator coupled to it, and combining the

intercalator coupled carrier substance, with a nucleic acid, to allow intercalation of the coupled intercalator and the nucleic acid. (Cl) further comprising a targeting molecule or transduction vector coupled to the carrier substance. The covalent coupling of the carrier substance to intercalator is a bioleavable linkage chosen from a hydrazine linkage, disulfide linkage, protected disulfide linkage, ester linkage, ortho ester linkage, phosphonamide linkage, bioleavable polypeptide, aromatic azo linkage and aldehyde bond. (Cl) further comprising a chloroquine substance coupled to the carrier substance. The carrier substance is chosen from avidins, streptavidins, liposomes, micelles and dendrimers. The method further involves coupling targeting molecule or transduction vector to the carrier substance, or coupling chloroquine substance to the carrier. (Cl) is useful for delivering nucleic acids for therapeutic or other medicinal uses. (Cl) is useful for targeting the delivery of nucleic acids to their site of action. (Cl) delivers nucleic acids into site of action and improves their effectiveness. The present sequence represents a transduction peptide that can be used as the transduction vector in the method of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18

DB 1 RGGRLSYRRRFFSTGTGR 18

RESULT 21

AD5E1567
ID AD5E1567 standard; peptide; 19 AA.

XX AC AD5E1567;

DT 29-JAN-2004 (first entry)

DE Peptide #5 to transport cyclosporin compound across blood brain barrier.

XX neuroprotective; cerebroprotective; vulnery; hemostatic;
XX anticonvulsant; neuroleptic; thrombolytic; anticoagulant; vasotropic;
KW nontropic; antiparkinsonian; cytotatic; antidiabetic; antibacterial;
KW anti-HIV; ophthalmological; antinflammatory; virucide; protozoacide;
KW immunosuppressive; dermatological; antithyroid; antidote; antirheumatic;
KW antiarthritic; antipsoriatic; endocrine-General; cyclophilin inhibitor;
KW calcineurin inhibitor;
KW neurotoxic calcium-dependent enzyme cascade blocker;
KW mitochondrial stabilizer; cyclosporin; transporter; blood-brain barrier.

XX OS Synthetic.

XX PN W02003070755-A2.

XX PD 28-AUG-2003.

XX PF 24-FEB-2003; 2003WO-FR000591.

XX PR 22-FEB-2002; 2002FR-00002299.

XX PA (SYNT-) SYNT-EM.

XX PA (MAAS-) MAAS BIOLAB LLC.

XX P1 Mouchet P, Rees AR, Elmer E, Keep MF;

XX DR WPI; 2003-712609/67.

XX PT New cyclosporin derivatives, containing bonded peptide vector for
PT crossing blood-brain barrier, used for treating cerebral disorders such
PT as neurodegenerative diseases, cerebral trauma or cerebrovascular
PT accidents.

XX PS Disclosure; SEQ ID NO 5; 77pp; French.

XX

CC The invention relates novel cyclosporin compounds (I) comprise at least
CC one cyclosporin molecule (II) and at least one peptide vector (III)
CC capable of transporting (I) across the blood-brain barrier. (I) are used
CC for the treatment or prevention of: (i) acute neurological disorders,
CC e.g. due to traumatic cerebral lesions, spinal cord lesions, exposure to
CC radiation, chemotherapy, epilepsy, schizophrenia, cerebral or spinal
CC surgery, cerebrovascular accidents, embolic cerebrovascular accident,
CC global cerebral ischemia, ruptured aneurysms, subarachnoid hemorrhage,
CC diseases selected from Alzheimer's disease, Parkinson's disease,
CC Huntington's disease, Down syndrome, Charcot disease, spino-muscular
CC atrophy, bulbar paralysis, schizophrenia, Tourette syndrome, diffuse
CC cerebrocortical atrophy, Lewy body dementia, mesolimbocortical dementia,
CC thalamic degeneration, Pick disease, multisystem dementia, cortico-
CC striato-spinal degeneration, Shy-Drager syndrome, Richardson-Steele-
CC Olzewski syndrome, Parkinson-amyotrophic lateral sclerosis-Guam dementia
CC complex, post-polio syndrome, olivocerebellar atrophy, Friedreich
CC ataxia, paraneoplastic syndrome, traumatic chronic encephalopathy
CC (boxer's dementia), Wilson disease, Menke disease, Tay-Sachs gangliosidosis,
CC Krabbe disease, peripheral neuropathy, diabetic neuropathy or aging;
CC (iii) prion diseases, such as Creutzfeldt Jacob disease (CJD), atypic CJD,
CC kuru, scrapie or bovine spongiform encephalitis; (iv) retroviral
CC diseases, e.g. AIDS dementia, AIDS myelopathy, AIDS peripheral neuropathy
CC or tropical paraparesis; (v) visual and retinal disorders, e.g. glaucoma-
CC related degeneration, macular degeneration, diabetic degeneration,
CC diabetic retinopathy, degeneration-related inflammation, detached retina,
CC optical neuritis, optic nerve lesions, optical chiasm or optical tractus
CC and retinal lesions caused by photons, trauma, ischemia or elevated
CC intracranial pressure; (vi) viral and bacterial diseases associated with
CC encephalopathy, including herpetic, equine, post-vaccination, Japanese or
CC Nile encephalitis, meningitis, rabies, poliomyelitis, progressive
CC multifocal leuko-encephalopathy, subacute sclerotic panencephalitis,
CC cerebral malaria, Lyme disease or neurosyphilis; (vii) immunological
CC diseases, e.g. plaque sclerosis, Guillain-Barre syndrome, lupus
CC erythematosus or Graves disease; (viii) the effects of neurotoxins,
CC including aminoglycosides, chlorinated hydrocarbons, organophosphates,
CC insecticides, herbicides, paraquat, nerve gas, 1-methyl-4-phenyl-1,2,3,6-
CC tetrahydropyridine, rotenone, cyanide, carbon monoxide, methanol,
CC ethanol, mercury, arsenic, chemotherapeutic agents (e.g. methotrexate,
CC mercaptopurine, fluorouracil, nitrosoureas, hydroxyurea, cisplatin,
CC carboplatin, daunorubicin, etoposide, vincristine, vinblastine, taxol (or
CC derivatives) or cyclophosphamide) or corticosteroids; (ix) metabolic
CC encephalopathy, e.g. hepatic or uremic encephalopathy; (x) conditions
CC requiring induction of a non-immune state, e.g. transplantation of
CC organs, tissues or cells or immune or autoimmune diseases such as
CC rheumatoid arthritis, eczema, psoriasis or alopecia; or (xi))
CC chemotherapy-resistant tumors. This sequence is an example of the peptide
CC part of the compound.

XX SQ Sequence 19 AA;

Query Match 100.0%; Score 91; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18

DB 2 RGGRLSYRRRFFSTGTGR 19

RESULT 22

AD888700

ID AD888700 standard; peptide; 19 AA.

XX AC AD888700;

XX

DT 18-NOV-2004 (first entry)

XX Amino acid sequence of a peptide designated Gly-SynB1.

XX disease treatment; active substance transport; bioavailability;
KW Gly-SynB1; cyclosporin A.

XX OS Unidentified.
XX PN FR2851471-A1.
XX PD 27-AUG-2004.
XX PF 24-FEB-2003; 2003FR-00002242.
XX PR 24-FEB-2003; 2003FR-00002242.
XX PA (SYNT-) SYNT:EM SA.
XX PI Rees AR, Mouchet P;
XX DR WPI; 2004-627939/61.
XX CC Compound comprising active agent coupled to vector through a linker,
XX PT useful in human or veterinary medicine, where the linker includes a
XX PT hydroxyproline residue.
XX PS Disclosure; SEQ ID NO 5; 65pp; French.
XX CC The specification describes a compound comprising at least one active
XX CC substance and at least one vector, connected by a linker that includes a
XX CC hydroxyproline residue. The linker is of a formula given in the
XX CC specification. The vector modifies the physicochemical or pharmacokinetic
XX CC properties of the active substance. The active substance is a protein,
XX CC (poly)peptide, antibody (or fragment), nucleic acid, oligonucleotide,
XX CC ribozyme, or a chemical for treatment or prevention of human or animal
XX CC disease, e.g. an antitumour or antiviral agent. Alternatively, it is a
XX CC radioactive or coloured material, or some other substance suitable as
XX CC indicator of metabolism or disease. Compounds of the invention are used
XX CC for treatment, prevention and diagnosis of disease in human or veterinary
XX CC medicine. They facilitate transport of the active substance across
XX CC biological barriers and its penetration into cells, and they also modify
XX CC the bioavailability or solubility of active substances. The present
XX CC sequence represents a peptide designated Gly-Synbl. Gly-Synbl was joined
XX CC to cyclosporin A via a linker to produce exemplary compounds of the
XX CC invention.
XX SQ Sequence 19 AA;
Query Match 100.0%; Score 91; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGGRLSYRRRSTSTGR 18
DB 2 RGGRLSYRRRSTSTGR 19
RESULT 23
AAW99403
ID AAW99403 standard; peptide; 18 AA.
XX AC AAW99403;
XX DT 08-JUN-1999 (first entry)
XX DE Protegrin derivative peptide SMI738.
XX KW Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure;
XX KW disulphide bridge; antibody; ribozyme; antitumour agent; antiviral;
XX KW anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;
XX KW nucleus; blood-brain barrier.
XX OS Synthetic.
XX PN WO9907728-A2.
XX PD 18-FEB-1999.
XX

PF 06-AUG-1998; 98WO-FR001757.
XX 12-AUG-1997; 97FR-00010297.
XX PA (SYNT-) SYNT:EM SA.
XX PI Calas B, Grassy G, Chavanieu A, Kaczorek M;
XX DR WPI; 1999-190034/16.
XX CC Derivatives of antibiotic peptides lacking disulfide bridges - used as
XX PT carriers to deliver active agents into cells.
XX PS Claim 7; Page 28; 37pp; French.
XX CC This peptide represents a linear derivative of the protegrin family of
XX CC peptide antibiotics. Protegrin antibiotics form part of the peptide
XX CC antibiotic family which contain a beta-sheet secondary structure linked
XX CC by disulphide bridges. The new derivatives are linear and lack the
XX CC disulphide bridge. The novel derivatives are used to deliver active
XX CC agents to an organism, e.g. therapeutic proteins, antibodies (or their
XX CC fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents,
XX CC antivirals and anti-inflammatories, etc. The derivatives are non-toxic
XX CC and non-lytic but can cross mammalian cell membranes rapidly by a passive
XX CC mechanism, so can deliver active agents to cytoplasm and nucleus,
XX CC including crossing the blood-brain barrier
XX SQ Sequence 18 AA;
Query Match 89.0%; Score 81; DB 2; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.5e-06;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 RGGRLSYRRRSTSTGR 18
DB 1 RGGRLSYRRRSTSTGR 18
RESULT 24
AAW93616
ID AAW93616 standard; peptide; 18 AA.
XX AC AAW93616;
XX DT 25-SEP-2000 (first entry)
XX DE Peptide which may be linked to anticancer agents.
XX KW Anticancer agent; cancer cell; resistance; P-glycoprotein pump; cancer.
XX OS Unidentified.
XX PN WO200032237-A1.
XX PD 08-JUN-2000.
XX PF 26-NOV-1999; 99WO-FR002939.
XX PR 30-NOV-1998; 98FR-00015073.
XX PA (SYNT-) SYNT:EM SA.
XX PI Temsamani J, Kaczorek M, Colin De Verdiere A;
XX DR WPI; 2000-412166/35.
XX PT New composition useful for cancer treatment and prevention, contains
XX PT anticancer agent and peptide vector that transports agent into cells.
XX PS Disclosure; Page 8; 34pp; French.
XX CC The specification describes a pharmaceutical composition, which comprises
XX CC at least one anticancer agent associated with at least one peptide that

CC can transport it into cancer cells and which inhibits development of
 CC resistance to the anticancer agent. By using the peptide as a vector for
 CC delivery of the anticancer agent, mechanisms that cause cancer cells to
 CC become resistant to the agent, particularly the P-glycoprotein pump, are
 CC avoided. Also, peptides are easily produced by chemical synthesis, can be
 CC coupled easily to the agent, cross mammalian cell membranes rapidly by a
 CC passive mechanism (no receptors required), and are non-toxic and non-
 CC lytic. The compositions are used to treat cancer. The present sequence
 CC represents a peptide which may be linked to the anticancer agents of the
 CC invention
 XX
 XX SQ Sequence 18 AA;

Query Match 89.0%; Score 81; DB 3; Length 18;
 Best Local Similarity 88.9%; Pred. No. 7.5e-06;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRPFSTGTGR 18
 DB 1 RGGRLSYRRRPFVSVGR 18

RESULT 25
 ABR43977
 ID ABR43977 standard; peptide; 18 AA.

AC ABR43977;
 DT 11-AUG-2003 (first entry)
 XX Beta-stranded antibiotic peptide linear derivative.
 XX Antibiotic; antigen; immunostimulant; vaccine; immune response.

OS Synthetic.
 XX WO2003033021-A1.
 XX 24-APR-2003.

XX 15-OCT-2002; 2002WO-EP011500.
 XX 16-OCT-2001; 2001EP-00402671.
 XX (SYNT-) SYNT:EM SA.

XX Johnson ME, Hamilton Day F, Kaczorek M, Tamsamani J;
 XX WPI; 2003-430304/40.

XX New conjugates of antigens, which are coupled to a linear derivative of a
 PT beta-stranded antibiotic peptide, useful for enhancing the immune
 PT response of a mammal to an antigen, particularly useful in vaccination or
 PT prophylaxis.

XX Claim 7; Page 27; 57pp; English.

XX The invention relates to a conjugate of an antigen, which is coupled to a
 CC linear derivative of a beta-stranded antibiotic peptide. The conjugate is
 CC useful for enhancing the immune response of a mammal to an antigen. The
 CC conjugate is particularly useful in vaccination or prophylaxis. The
 CC present sequence represents a linear derivative of a beta-stranded
 CC antibiotic peptide

XX Sequence 18 AA;

Query Match 89.0%; Score 81; DB 6; Length 18;
 Best Local Similarity 88.9%; Pred. No. 7.5e-06;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRPFSTGTGR 18
 DB 1 RGGRLSYRRRPFVSVGR 18

RESULT 26
 ADN03481

ID ADN03481 standard; peptide; 18 AA.

AC ADN03481;

XX 01-JUL-2004 (first entry)

XX Beta-stranded proteogrin peptide linear deriative #4.

XX Beta-stranded antibiotic peptide; immune response; therapy; vaccine;
 XX proteogrin.

OS Unidentified.

XX US2004072340-A1.

XX 15-APR-2004.

XX 15-OCT-2002; 2002US-00270010.

XX 15-OCT-2002; 2002US-00270010.

XX (JOHN/) JOHNSON M E.

XX (DAYF/) HAMILTON DAY F.

XX (KACZ/) KACZOREK M.

XX (TEMS/) TEMSAMANI J.

XX Johnson ME, Hamilton Day F, Kaczorek M, Tamsamani J;
 XX WPI; 2004-328576/30.

XX New conjugates of an antigen coupled to a linear derivative of a beta-
 PT stranded antibiotic peptide, useful for enhancing the immune response of
 PT a mammal to an antigen.

XX Claim 7; SEQ ID NO 7; 21pp; English.

XX The present invention relates to conjugates of an antigen coupled to a
 CC linear derivative of a beta-stranded antibiotic peptide. The invention is
 CC useful for enhancing the immune response of a mammal to an antigen. The
 CC invention is also useful in the production of vaccines. The present
 CC sequence is a beta-stranded proteogrin (antibiotic) peptide linear
 CC derivative.

XX Sequence 18 AA;

Query Match 89.0%; Score 81; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 7.5e-06;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRPFSTGTGR 18
 DB 1 RGGRLSYRRRPFVSVGR 18

RESULT 27
 AAE29879

ID AAE29879 standard; peptide; 18 AA.

AC AAE29879;

XX 24-FEB-2003 (first entry)

XX Membrane translocation peptide, penetratin.

XX Gonadotrophin releasing hormone analogue; neurotoxin; prostate cancer;
 XX endocrine disorder; gonadotrophin related illness; endometrial cancer;
 XX pancreatic cancer; breast cancer; endometriosis; precocious puberty;
 XX GnRH-A; therapy; penetratin.

XX	Antibiotic peptide PG-4A.
DE	
XX	Amphipathic peptide; antibiotic peptide; carrier.
KW	
XX	Synthetic.
OS	
XX	WO200202595-A1.
FN	
XX	10-JAN-2002.
PD	
XX	03-JUL-2001; 2001WO-FR002129.
PF	
XX	03-JUL-2000; 2000FR-00008633.
PR	
XX	(SYNT-) SYNT:EM SA.
XX	
PI	Drin G, Gomar J, Tamsamani J, Rees AR;
XX	
DR	WPI; 2002-241369/29.
XX	
PT	New amphipathic derivatives of antibiotic peptides, are useful for
PT	delivering therapeutic and diagnostic agents to cells, provides efficient
PT	transport across membranes.
XX	
PS	Claim 8; Page 24; 49pp; French.
XX	
CC	The present invention related to novel amphipathic antibiotic peptides.
CC	The present sequence is one such peptide. The peptides are useful as
CC	carriers for delivering attached active agents to cells, specifically to
CC	a target site in cytoplasm or the nucleus, for therapeutic or diagnostic
CC	use
XX	
XX	Sequence 18 AA;
XX	
XX	Query Match 75.8%; Score 69; DB 5; Length 18;
XX	Best Local Similarity 66.7%; Pred. No. 0.00064;
XX	Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY	1 RGGRLSYSRPRFSTSTGR 18
DB	1 RGGRLAYRRRFAVAVGR 18
DB	: :
DB	: :
DB	1 RGGRLAYRRRFAVAVGR 18
DB	
DB	RESULT 32
AAW18153	
ID	AAW18153 standard; peptide; 18 AA.
AC	
XX	AAW18153;
XX	
XX	25-MAR-2003 (revised)
DT	
DT	11-AUG-1997 (first entry)
XX	
DB	Cationic, antimicrobial, virus-neutralising protegrin PC-57.
XX	
KW	Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
KW	Candida albicans; gram-negative bacteria; STD;
KW	sexually transmitted disease; HIV-1; Chlamydia trachomatis;
KW	Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative; food.
XX	
OS	Synthetic.
XX	
XX	WO9637508-A1.
XX	
XX	28-NOV-1996.
PD	
XX	24-MAY-1996; 96WO-US0007594.
XX	
XX	26-MAY-1995; 95US-00451832.
PR	
PR	07-JUL-1995; 95US-00499523.
XX	
XX	(REGC) UNIV CALIFORNIA.
XX	

```
PI  Lehrer RI, Kokryakov VN, Harwig SS;
XX  WPI; 1997-033984/03.
XX
XX  Cationic, antimicrobial, virus-neutralising protegrin peptide(s) - useful
PT  for the treatment of microbial infection, as food preservatives and in
PT  eye care solutions.
XX
XX  Claim 6; Page 64; 106pp; English.
XX
XX  The present sequence is a specifically claimed example of a peptide,
CC  recombinantly produced, corresponding to the generic formula: A1-A2-A3-A4
CC  -A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16- (A17-A18) where A1 = a
CC  basic amino acid; A2 and A3 = a small amino acid; A4 = a basic or small
CC  amino acid; A5, A7 and A14 = a hydrophobic amino acid; A9, A12 and A16 =
CC  a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a
CC  basic, hydrophobic, neutral/polar or small amino acid or proline; A17 may
CC  be absent or a basic, neutral/polar, hydrophobic or small amino acid; and
CC  A18 may be absent or a basic, neutral/polar, hydrophobic or small amino
CC  acid. This has a charge of at least +3 and its N-terminal acylated and/or
CC  C-terminal amidated or esterified forms, all of which may contain a
CC  disulphide bond to give a cysteine bridge. This peptide is in snake form
CC  where all the cysteine residues are replaced by a hydrophobic, small or
CC  large polar amino acid (e.g. alanine in this case). Peptides of this
CC  formula are designated protegrins and are useful as anti-bacterial, anti-
CC  viral and anti-fungal agents in plants and animals. The protegrins confer
CC  resistance to microbial or viral infection in plants by preventing the
CC  growth of a virus or microbe and inactivate the endotoxin of gram-
CC  negative bacteria. The protegrins are particularly useful for the
CC  treatment of sexually transmitted disease caused by microorganisms e.g.
CC  Candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and
CC  Neisseria gonorrhoeae. They can also be used in eye care solutions and as
CC  preservatives for food. The protegrins are more effective under
CC  physiological conditions (e.g. in the presence of serum) than certain
CC  antibiotics and are non-toxic to the cells of higher organisms. (Updated
CC  on 25-MAR-2003 to correct PA field.)
XX
XX  Sequence 18 AA;
XX
XX  Query Match 73.6%; Score 67; DB 2; Length 18;
XX  Best Local Similarity 66.7%; Pred. No. 0.0013;
XX  Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY  1 RGGRLSYSRRRSTSTGR 18
DB  |||||:||||: ||
    1 RGGRLAYARRRFAVWGR 18

RESULT 33
ADL18453
XX  ADL18453 standard; peptide; 18 AA.
XX
XX  ADL18453;
XX  AC
XX  XX
XX  06-MAY-2004 (first entry)
XX
XX  Antimicrobial protegrin peptide PC-57.
XX
XX  virucide; antimicrobial; peptide therapy; recombinant peptide compound;
XX  antiviral; viral infection; microbial infection; endotoxin inactivation;
XX  eye care; contact lens solution; topical composition;
XX  pharmaceutical composition; sexually transmitted disease; STD; protegrin.
XX
XX  Synthetic.
XX
XX  Key Location/Qualifiers
XX  Modified-site 18
XX  /label= OTHER
XX  /note= "OTHER= C-terminal amidation"
XX
XX  US6653442-B1.
XX
XX  25-NOV-2003.
XX
XX  PD

Lehrer RI, Chen J, Steinberg DA, Lehrer RI, Harwig SS;
Kokryakov VN;
WPI; 2004-068297/07.
New peptide in its N-terminal acylated or C-terminal amidated or
esterified form in linear or cysteine-bridged form, useful for treating
sexually transmitted diseases and as preservatives.
Claim 1; SEQ ID NO 93; 84pp; English.
The invention describes a purified and isolated or recombinantly produced
peptide compound selected from any of the 43 fully defined sequences of
16-18 amino acids, given in the specification, or its N-terminal acylated
or C-terminal amidated or esterified forms in linear or cysteine-bridged
form. Also described are: a pharmaceutical composition for antimicrobial
or antiviral use, comprising any of the peptides cited above in admixture
with at least one excipient; and a composition for application to plants
or plant environments for conferring resistance to microbial or viral
infections in plants comprising any of the peptides cited above in
admixture with at least one diluent. The peptides are useful as
preservatives and in preventing, treating or ameliorating viral or
microbial infections in animals and plants, and in inactivating
endotoxins. They are particularly useful in eye care, such as in contact
lens solutions, and in topical and pharmaceutical compositions for
treating sexually transmitted diseases (STDs). This is the amino acid
sequence of an antimicrobial protegrin peptide of the invention.
XX
XX  Sequence 18 AA;
XX
XX  Query Match 73.6%; Score 67; DB 8; Length 18;
XX  Best Local Similarity 66.7%; Pred. No. 0.0013;
XX  Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY  1 RGGRLSYSRRRSTSTGR 18
DB  |||||:||||: ||
    1 RGGRLAYARRRFAVWGR 18

RESULT 34
AAY22007
XX  AAY22007 standard; peptide; 18 AA.
XX
XX  AC
XX  AAY22007;
XX
XX  23-AUG-1999 (first entry)
XX
XX  Antimicrobial peptide derivative of protegrin.
XX
XX  Antimicrobial peptide; protegrin; microbe growth inhibitor; Pseudomonas;
XX  microbial infection; Staphylococcus aureus; Helicobacter pylori; therapy;
XX  antibiotic-resistant bacterium; disinfectant composition; preservative;
XX  haemolytic activity; systemic antibiotic.
XX
XX  Sus scrofa.
XX
XX  WO9927945-A1.
XX
XX  10-JUN-1999.
XX
XX  PD
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XX PF 01-DEC-1998; 98WO-US025458.
XX XX
XX PR 03-DEC-1997; 97US-00984294.
XX XX
XX PA (INTR-) INTRABIOTICS PHARM INC.
XX XX
XX PI Chang CC, Chen J, Lehrer RI, Radel PA;
XX DR WPI; 1999-385321/32.
XX XX
XX PT Antimicrobial threonine-containing protegrins.
XX XX
XX PS Claim 11; Page 52; 75pp; English.
XX XX
XX CC This sequence represents an example of an antimicrobial peptide (I) of
XX CC the invention, and comprises 10-30 amino acid residues based on a
XX CC naturally-occurring protegrin peptide. The antimicrobial peptide is
XX CC useful in environmental composition for application to plants or plant
XX CC environments, for inhibiting the growth of microbes. The peptide is
XX CC useful for treating or preventing microbial infections, e.g. caused by
XX CC Staphylococcus aureus, Pseudomonas, Helicobacter pylori or an antibiotic-
XX CC resistant bacterium, or related diseases. The peptide can be used to
XX CC inactivate the endotoxin of Gram-negative bacteria. The peptides can be
XX CC used in disinfectant compositions, and as preservatives for materials
XX CC such as foodstuffs, cosmetics, medicaments or other materials containing
XX CC nutrients for organisms. The peptides exhibit decreased haemolytic
XX CC activity against human red blood cells as compared with native PG-1 and
XX CC melittin. They have improved serum compatibility and therefore improved
XX CC use as systemic antibiotics. At the same time the peptides provide broad
XX CC spectrum activity with a low frequency of resistance
XX SQ Sequence 18 AA;

Query Match 72.5%; Score 66; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.002;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RGGRLSYSRRRFSTGCR 18
Db ||||| ||||| |||
1 RGGRLCYCRRRFFCTGCR 18

RESULT 36
AAW36429
ID AAW36429 standard; peptide; 18 AA.
XX AC AAW36429;
XX XX
DT 13-FEB-1998 (first entry)
XX XX
DE Antimicrobial protegrin peptide (229).
XX XX
XX KW Antimicrobial protegrin; broad spectrum; gram-positive; bacterium;
XX KW gram-negative; bacteria; yeast; fungus; protozoa; virus;
XX KW retrovirus; HIV; human immunodeficiency virus; preservation;
XX KW disinfection; prophylaxis; treatment; infection; disease; conjunctivitis;
XX KW keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori;
XX KW sexually transmitted disease; oral mucositis; gram-negative sepsis;
XX KW endocarditis; pneumonia; biocidal; biostatic; respiratory infection;
XX KW urinary tract infection; MRSA; protozoan;
XX KW vancomycin resistant Enterococcus; pathogen; multi-drug resistance;
XX KW penicillin resistant Streptococcus pneumoniae; pig; porcine;
XX KW methicillin resistant Staphylococcus aureus; systemic candidiasis.
XX OS Synthetic.
XX OS Sus scrofa.
XX XX
XX PN WO9718826-A1.
XX XX
XX PD 29-MAY-1997.
XX XX
XX PF 22-NOV-1996; 96WO-US018544.
XX XX
XX PR 22-NOV-1995; 95US-00562346.
XX PR 17-MAY-1996; 96US-00649811.
XX PR 01-AUG-1996; 96US-00690921.
XX PR 21-NOV-1996; 96US-00752852.
XX XX
XX PA (INTR-) INTRABIOTICS PHARM INC.
XX PA (REGC) UNIV CALIFORNIA.
XX XX
XX PI Chang CC, Gu CL, Chen J, Steinberg DA, Lehrer RI;
XX DR WPI; 1999-385321/32.

XX PF 01-DEC-1998; 98WO-US025458.
XX XX
XX PR 03-DEC-1997; 97US-00984294.
XX XX
XX PA (INTR-) INTRABIOTICS PHARM INC.
XX XX
XX PI Chang CC, Chen J, Lehrer RI, Radel PA;
XX DR WPI; 1999-385321/32.

XX PF 01-DEC-1998; 98WO-US025458.
XX XX
XX PR 03-DEC-1997; 97US-00984294.
XX XX
XX PA (INTR-) INTRABIOTICS PHARM INC.
XX XX
XX PI Chang CC, Chen J, Lehrer RI, Radel PA;
XX DR WPI; 1999-385321/32.

Query Match 72.5%; Score 66; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.002;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RGGRLSYSRRRFSTGCR 18
Db ||||| ||||| |||
1 RGGRLCYCRRRFFCTGCR 18

RESULT 35
AAW22005
ID AAW22005 standard; peptide; 18 AA.
XX AC AAW22005;
XX XX
DT 23-AUG-1999 (first entry)
XX XX
DE Antimicrobial peptide derivative of protegrin.
XX XX
XX KW Antimicrobial peptide; protegrin; microbe growth inhibitor; Pseudomonas;
XX KW microbial infection; Staphylococcus aureus; Helicobacter pylori; therapy;
XX KW antibiotic-resistant bacterium; disinfectant composition; preservative;
XX KW haemolytic activity; systemic antibiotic.
XX OS Sus scrofa.
XX XX
XX PN WO9927945-A1.
XX XX
XX PD 10-JUN-1999.
XX XX
XX PF 01-DEC-1998; 98WO-US025458.
XX XX
XX PR 03-DEC-1997; 97US-00984294.
XX XX
XX PA (INTR-) INTRABIOTICS PHARM INC.
XX XX
XX PI Chang CC, Chen J, Lehrer RI, Radel PA;
XX DR WPI; 1999-385321/32.

```

XX WPI; 1997-297871/27.
 XX
 XX
 PT New antimicrobial protegrin peptide(s) - having activity against
 PT bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g.
 PT HIV).
 XX
 XX
 PS Claim 23; Page 110; 130pp; English.
 XX
 XX The present sequence is an antimicrobial protegrin peptide, which has a
 CC broad spectrum of activity against microbial targets, including gram-
 CC positive and gram-negative bacteria, yeast, fungi, protozoa and certain
 CC strains of viruses and retroviruses, e.g. HIV. It can be used to preserve
 CC or disinfect a variety of materials, including medical equipment.
 CC foodstuffs, cosmetics, contact lens solutions, medicaments or other
 CC nutrient containing materials. It can also be used for the prophylaxis or
 CC treatment of microbial infections or diseases in plants and animals, e.g.
 CC conjunctivitis, keratitis, corneal ulcers, stomach ulcers associated with
 CC Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis,
 CC endocarditis, pneumonia and other respiratory infections, urinary tract
 CC infections, systemic candidiasis and oral mucositis. It is biostatic or
 CC biocidal against clinically relevant pathogens exhibiting multi-drug
 CC resistance, e.g. vancomycin resistant Enterococcus faecium or faecalis,
 CC penicillin resistant Streptococcus pneumoniae and methicillin resistant
 CC Staphylococcus aureus (MRSA). It is given at a dosage of 0.1 to 5,
 CC preferably 0.5 to 1 mg/kg/day, by injection
 XX
 SQ Sequence 18 AA;
 Query Match 71.4%; Score 65; DB 2; Length 18;
 Best Local Similarity 66.7%; Pred. No. 0.0028;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 RGRGLYSRRRPFSTGTGR 18
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 Db 1 RGRGLCYARRRFAVCVGR 18
 RESULT 37
 AAW09085
 ID AAW09085 standard; peptide; 18 AA.
 AC AAW09085;
 DT 25-MAR-2003 (revised)
 DT 11-AUG-1997 (first entry)
 XX
 XX Cationic, antimicrobial, virus-neutralising protegrin IB-289.
 XX
 XX Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
 KW Candida albicans; gram-negative bacteria; STD;
 KW sexually transmitted disease; HIV-1; Chlamydia trachomatis;
 KW Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative; food.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "Acylated"
 FT Disulfide-bond 6..15
 FT /note= "results in bullet form peptide"
 FT Modified-site 18
 FT /note= "Amidated"
 XX
 XX WO9637508-A1.
 PN
 XX
 PD 28-NOV-1996.
 XX
 PF 24-MAY-1996; 96WO-US0007594.
 XX
 XX 26-MAY-1995; 95US-00451832.
 PR 07-JUL-1995; 95US-00499523.
 PR
 XX

(REGC) UNIV CALIFORNIA.
 PI Lehrer RI, Kokryakov VN, Harwig SS;
 XX WPI; 1997-033984/03.
 XX
 XX Cationic, antimicrobial, virus-neutralising protegrin peptide(s) - useful
 PT for the treatment of microbial infection, as food preservatives and in
 PT eye care solutions.
 XX
 XX Claim 6; Page 65; 106pp; English.
 PS
 XX The present sequence is a specifically claimed example of a peptide,
 CC recombinantly produced, corresponding to the generic formula: A1-A2-A3-A4
 CC -A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18) where A1 = a
 CC basic amino acid; A2 and A3 = a small amino acid; A4 = a basic or small
 CC amino acid; A5, A7 and A14 = a hydrophobic amino acid; A9, A12 and A16 =
 CC a basic, hydrophobic, neutral/polar or small amino acid or proline; A17 may
 CC be absent or a basic, neutral/polar, hydrophobic or small amino acid; and
 CC A18 may be absent or a basic, neutral/polar, hydrophobic or small amino
 CC acid. This has a charge of at least +3 and its N-terminal acylated and/or
 CC C-terminal amidated or esterified forms, all of which may contain a
 CC disulphide bond to give a cysteine bridge. Peptides of this formula are
 CC designated protegrins and are useful as anti-bacterial, anti-viral and
 CC anti-fungal agents in plants and animals. The protegrins confer
 CC resistance to microbial or viral infection in plants by preventing the
 CC growth of a virus or microbe and inactivate the endotoxin of gram-
 CC negative bacteria. The protegrins are particularly useful for the
 CC treatment of sexually transmitted disease caused by microorganisms e.g.
 CC Candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and
 CC Neisseria gonorrhoeae. They can also be used in eye care solutions and as
 CC preservatives for food. The protegrins are more effective under
 CC physiological conditions (e.g. in the presence of serum) than certain
 CC antibiotics and are non-toxic to the cells of higher organisms. (Updated
 CC on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 18 AA;
 Query Match 71.4%; Score 65; DB 2; Length 18;
 Best Local Similarity 66.7%; Pred. No. 0.0028;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 RGRGLYSRRRPFSTGTGR 18
 ||||| :|||: ||
 Db 1 RGRGLCYARRRFAVCVGR 18
 RESULT 38
 AAW09084
 ID AAW09084 standard; peptide; 18 AA.
 XX
 AC AAW09084;
 XX
 DT 25-MAR-2003 (revised)
 DT 11-AUG-1997 (first entry)
 XX
 XX Cationic, antimicrobial, virus-neutralising protegrin IB-288.
 DE
 XX Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
 KW Candida albicans; gram-negative bacteria; STD;
 KW sexually transmitted disease; HIV-1; Chlamydia trachomatis;
 KW Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative; food.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "Acylated"
 FT Disulfide-bond 6..15
 FT /note= "results in bullet form peptide"
 FT Modified-site 18
 FT /note= "Amidated"
 XX
 XX WO9637508-A1.
 PN
 XX
 PD 28-NOV-1996.
 XX
 PF 24-MAY-1996; 96WO-US0007594.
 XX
 XX 26-MAY-1995; 95US-00451832.
 PR 07-JUL-1995; 95US-00499523.
 PR
 XX

XX PD 28-NOV-1996.
 XX PF 24-MAY-1996; 96WO-US007594.
 XX PR 26-MAY-1995; 95US-00451832.
 XX PR 07-JUL-1995; 95US-00499523.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Lehrer RI, Kokryakov VN, Harwig SS;
 XX DR WPI; 1997-033984/03.
 XX PT Cationic, antimicrobial, virus-neutralising protegrin peptide(s) - useful
 PT for the treatment of microbial infection, as food preservatives and in
 PT eye care solutions.
 XX PS Claim 6; Page 65; 106pp; English.
 XX CC The present sequence is a specifically claimed example of a peptide,
 CC recombinantly produced, corresponding to the generic formula: A1-A2-A3-A4
 CC -A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16- (A17-A18) where A1 = a
 CC basic amino acid; A2 and A3 = a small amino acid; A4 = a basic or small
 CC amino acid; A5, A7 and A14 = a hydrophobic amino acid; A9, A12 and A16 =
 CC a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a
 CC basic, hydrophobic, neutral/polar or small amino acid or proline; A17 may
 CC be absent or a basic, neutral/polar, hydrophobic or small amino acid; and
 CC A18 may be absent or a basic, neutral/polar, hydrophobic or small amino
 CC acid. This has a charge of at least +3 and its N-terminal acylated and/or
 CC C-terminal amidated or esterified forms, all of which may contain a
 CC disulphide bond to give a cysteine bridge. Peptides of this formula are
 CC designated protegrins and are useful as anti-bacterial, anti-viral and
 CC anti-fungal agents in plants and animals. The protegrins confer
 CC resistance to microbial or viral infection in plants by preventing the
 CC growth of a virus or microbe and inactivate in plants by preventing the
 CC negative bacteria. The protegrins are particularly useful for the
 CC treatment of sexually transmitted disease caused by microorganisms e.g.
 CC Candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and
 CC Neisseria gonorrhoeae. They can also be used in eye care solutions and as
 CC preservatives for food. The protegrins are more effective under
 CC physiological conditions (e.g. in the presence of serum) than certain
 CC antibiotics and are non-toxic to the cells of higher organisms. (Updated
 CC on 25-MAR-2003 to correct PA field.)
 XX SQ Sequence 18 AA;
 Query Match 71.4%; Score 65; DB 2; Length 18;
 Best Local Similarity 66.7%; Pred. No. 0.0028;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 RGRGLSYRRRFFSTGTGR 18
 ||||| :|||: ||
 Db 1 RGRGLCYARRRFAVCVGR 18
 RESULT 39
 ADL18459
 ID ADL18459 standard; peptide; 18 AA.
 XX AC ADL18459;
 XX DT 06-MAY-2004 (first entry)
 XX DE Antimicrobial protegrin peptide IB-288.
 XX virucide; antimicrobial; peptide therapy; recombinant peptide compound;
 KW antiviral; viral infection; microbial infection; endotoxin inactivation;
 KW eye care; contact lens solution; topical composition;
 KW pharmaceutical composition; sexually transmitted disease; STD; protegrin.
 XX OS Synthetic.
 XX

PN US6653442-B1.
 XX 25-NOV-2003.
 XX PF 30-AUG-1999; 99US-00385328.
 XX PR 20-JUL-1993; 93US-00093926.
 PR 26-JUL-1993; 93US-00095769.
 PR 13-JAN-1994; 94US-00182483.
 PR 17-MAY-1994; 94US-00243879.
 PR 07-JUL-1995; 95US-00499523.
 PR 24-MAY-1996; 96WO-US007594.
 PR 28-OCT-1996; 96US-00741860.
 PR 03-AUG-1998; 98US-00128345.
 XX (INTR-) INTRABIOTICS PHARM INC.
 XX Chang CC, Gu CL, Chen J, Steinberg DA, Lehrer RI, Harwig SSL;
 PI Kokryakov VN;
 XX WPI; 2004-068297/07.
 XX DR New peptide in its N-terminal acylated or C-terminal amidated or
 PT esterified form in linear or cysteine-bridged form, useful for treating
 PT sexually transmitted diseases and as preservatives.
 XX PS Claim 1; SEQ ID NO 99; 84pp; English.
 XX CC The invention describes a purified and isolated or recombinantly produced
 CC peptide compound selected from any of the 43 fully defined sequences of
 CC 16-18 amino acids, given in the specification, or its N-terminal acylated
 CC or C-terminal amidated or esterified forms in linear or cysteine-bridged
 CC form. Also described are: a pharmaceutical composition for antimicrobial
 CC or antiviral use, comprising any of the peptides cited above in admixture
 CC with at least one excipient; and a composition for application to plants
 CC or plant environments for conferring resistance to microbial or viral
 CC infections in plants comprising any of the peptides cited above in
 CC admixture with at least one diluent. The peptides are useful as
 CC preservatives and in preventing, treating or ameliorating viral or
 CC microbial infections in animals and plants, and in inactivating
 CC endotoxins. They are particularly useful in eye care, such as in contact
 CC lens solutions, and in topical and pharmaceutical compositions for
 CC treating sexually transmitted diseases (STDs). This is the amino acid
 CC sequence of an antimicrobial protegrin peptide of the invention.
 XX SQ Sequence 18 AA;
 Query Match 71.4%; Score 65; DB 8; Length 18;
 Best Local Similarity 66.7%; Pred. No. 0.0028;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 RGRGLSYRRRFFSTGTGR 18
 ||||| :|||: ||
 Db 1 RGRGLCYARRRFAVCVGR 18
 RESULT 40
 ADL18460
 ID ADL18460 standard; peptide; 18 AA.
 XX AC ADL18460;
 XX DT 06-MAY-2004 (first entry)
 XX DE Antimicrobial protegrin peptide IB-289.
 XX virucide; antimicrobial; peptide therapy; recombinant peptide compound;
 KW antiviral; viral infection; microbial infection; endotoxin inactivation;
 KW eye care; contact lens solution; topical composition;
 KW pharmaceutical composition; sexually transmitted disease; STD; protegrin.
 XX OS Synthetic.
 XX

FH Key Location/Qualifiers
 FT Modified-site 18
 FT /label= OTHER
 FT /note= "OTHER= C-terminal amidation"

XX US6653442-B1.

XX 25-NOV-2003.

XX 30-AUG-1999; 99US-00385328.

XX 20-JUL-1993; 93US-00093926.

XX 26-JUL-1993; 93US-00095769.

XX 13-JAN-1994; 94US-00182483.

XX 17-MAY-1994; 94US-00243879.

XX 07-JUL-1995; 95US-00499523.

XX 24-MAY-1996; 96WO-US007594.

XX 28-OCT-1996; 96US-00741860.

XX 03-AUG-1998; 98US-00128345.

XX (INTR-) INTRABIOTICS PHARM INC.

XX Chang CC, Gu CL, Chen J, Steinberg DA, Lehrer RI, Harwig SSL;

XX Kokryakov VN;

XX WPI; 2004-068297/07.

XX New peptide in its N-terminal acylated or C-terminal amidated or esterified form in linear or cysteine-bridged form, useful for treating sexually transmitted diseases and as preservatives.
 Claim 1; SEQ ID NO 100; 84pp; English.
 The invention describes a purified and isolated or recombinantly produced peptide compound selected from any of the 43 fully defined sequences of 16-18 amino acids, given in the specification, or its N-terminal acylated or C-terminal amidated or esterified forms in linear or cysteine-bridged form. Also described are: a pharmaceutical composition for antimicrobial or antiviral use, comprising any of the peptides cited above in admixture with at least one excipient; and a composition for application to plants or plant environments for conferring resistance to microbial or viral infections in plants comprising any of the peptides cited above in admixture with at least one diluent. The peptides are useful as preservatives and in preventing, treating or ameliorating viral or microbial infections in animals and plants, and in inactivating endotoxins. They are particularly useful in eye care, such as in contact lens solutions, and in topical and pharmaceutical compositions for treating sexually transmitted diseases (STDs). This is the amino acid sequence of an antimicrobial protegrin peptide of the invention.

SQ Sequence 18 AA;

Query Match 71.4%; Score 65; DB 8; Length 18;
 Best Local Similarity 66.7%; Pred. No. 0.0028;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RGRLLSYRRRFFSTGTGR 18

DB 1 RGRLLCYARRRFAVCVGR 18

Search completed: May 21, 2006, 00:19:03
 Job time : 199 secs

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(without alignments)
30.893 Million cell updates/sec

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Searched: 650591 seqs, 87530628 residues

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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 102, App
Sequence 107, App
Sequence 1, Appl
Sequence 2, Appl
Sequence 28, Appl
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Sequence 27, Appl
Sequence 11, Appl
Sequence 16, Appl
Sequence 33, Appl
Sequence 48, Appl
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Sequence 154, App
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Sequence 55, Appl

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ALIGNMENTS

RESULT 1

US-10-144-549-17
; Sequence 17, Application US/10144549
; Patent No. 6835810
; GENERAL INFORMATION:
; APPLICANT: GenShuttle Biopharm, Inc.
; APPLICANT: Hwu, Paul L.
; TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR
; FILE REFERENCE: MEHB 02-340
; CURRENT APPLICATION NUMBER: US/10/144,549
; CURRENT FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Membrane fusion sequence.
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Synthetic sequence from protegrins/procine leukocyte.
US-10-144-549-17

Query Match 100.0%; Score 91; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18
|||||:|||||
Db 1 RGGRLSYRRRFFSTGTGR 18

RESULT 2

US-09-810-601B-42
; Sequence 42, Application US/09810601B
; Patent No. 6831059
; GENERAL INFORMATION:
; APPLICANT: Allergan Sales, Inc.
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING GONADOTROPHIN RELATED ILLNE
; FILE REFERENCE: D-2947-CIP
; CURRENT APPLICATION NUMBER: US/09/810,601B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/692,811
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Membrane Translocation Peptide
US-09-810-601B-42

Query Match 87.9%; Score 80; DB 2; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.3e-06;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18
|||||:|||||
Db 1 RGGRLSYRRRFFSTGTGR 18

RESULT 3

US-09-385-328-93

; Sequence 93, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Gu, Chee L.
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehre, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakon, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT APPLICATION NUMBER: US/09/385,328
; CURRENT FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 09/128,345
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
US-09-385-328-93

Query Match 73.6%; Score 67; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.00038;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18
|||||:|||||
Db 1 RGGRLAYARRRFAVNGR 18

RESULT 4

US-08-984-294-6
; Sequence 6, Application US/08984294
; Patent No. 6043220
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Chen, Jie
; APPLICANT: Lehre, Robert I.
; TITLE OF INVENTION: THREONINE-CONTAINING PROTEGRINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of The Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,294
; FILING DATE: 03-DEC-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 008067-0049-999

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6043220e
US-08-984-294-6

Query Match 72.5%; Score 66; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.00055;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18
||||| ||||| |||||
Db 1 RGGRLCYRRRFFCTGVR 18

RESULT 5
US-08-984-294-8
Sequence 8, Application US/08984294
Patent No. 6043220
GENERAL INFORMATION:
APPLICANT: Chang, Conway C.
APPLICANT: Chen, Jie
APPLICANT: Lehrer, Robert I.
TITLE OF INVENTION: THREONINE-CONTAINING PROTEGRINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,294
FILING DATE: 03-DEC-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 008067-0049-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6043220e
US-08-984-294-8

Query Match 72.5%; Score 66; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.00055;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18

Db 1 RGGRLCYRRRFFCTGVR 18
||||| ||||| ||||| |||||

RESULT 6
US-08-499-523-63
Sequence 63, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: group(6, 8, 13, 15)
OTHER INFORMATION: /note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-63

Query Match 71.4%; Score 65; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0008; 6; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18
||||| ||||| ||||| |||||
Db 1 RGGRLXYRRRFFXVGR 18

RESULT 7
US-08-499-523-67
Sequence 67, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500

;
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/499,523
; FILING DATE: 07-JUL-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: group(6, 8, 13, 15)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-67

Query Match 71.4%; Score 65; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0008; 6; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGRGLYSRRRSTSTGR 18
||||| :||| :||
Db 1 RGRGLYXRRRFXVXVGR 18
RESULT 8
US-08-752-852A-230
; Sequence 230, Application US/08752852A
; Patent No. 5994306
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Chee-Liang
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah
; APPLICANT: Lehrer, Robert
; APPLICANT: Harwig, Sylvia
; TITLE OF INVENTION: FINS-TUNED PROTEGRINS
; NUMBER OF SEQUENCES: 242
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,852A
; FILING DATE: 21-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

;
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-034-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 230:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-752-852A-230
Query Match 71.4%; Score 65; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0008; 4; Indels 0; Gaps 0;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 RGRGLYSRRRSTSTGR 18
||||| :||| :||
Db 1 RGRGLCYARRRFAVCVGR 18
RESULT 9
US-09-128-345-63
; Sequence 63, Application US/09128345
; Patent No. 6159936
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: group(6, 8, 13, 15)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"

US-09-128-345-63

Query Match 71.4%; Score 65; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0008;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGTGR 18
Db 1 RGGRLXYRRRPFVXVGR 18

RESULT 10

US-09-128-345-67
; Sequence 67, Application US/09128345
; Patent No. 6159936
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S. L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura, A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: group(6, 8, 13, 15)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"

US-09-128-345-67

Query Match 71.4%; Score 65; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0008;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGTGR 18
Db 1 RGGRLXYRRRPFVXVGR 18

RESULT 11

US-09-385-328-99
; Sequence 99, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.

; APPLICANT: Gu, Chee L.
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakov, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT APPLICATION NUMBER: US/09/385,328
; CURRENT FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 09/128,345
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-385-328-99

Query Match 71.4%; Score 65; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0008;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGTGR 18
Db 1 RGGRLCYARRRFAVCVGR 18

RESULT 12

US-09-385-328-100
; Sequence 100, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Gu, Chee L.
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakov, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT APPLICATION NUMBER: US/09/385,328
; CURRENT FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 09/128,345
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
US-09-385-328-100

Query Match 71.4%; Score 65; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0008;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGTGR 18
Db 1 RGGRLCYARRRFAVCVGR 18

```
RESULT 13
US-09-385-328-111
; Sequence 91, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Gu, Chee L.
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakov, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT APPLICATION NUMBER: US/09/385,328
; CURRENT FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 09/128,345
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
; LOCATION: 18
; NAME/KEY: SITE
; LOCATION: 6, 8, 13, 15
; OTHER INFORMATION: Xaa = hydrophobic, small or large polar amino acid
US-09-385-328-111

Query Match      71.4%; Score 65; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0008;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 RGRLSYSRRRPFSTGTGR 18
      ||||| | |||| | ||
DB      1 RGRGLXRRRFXVXVGR 18

RESULT 14
US-09-385-328-91
; Sequence 91, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Gu, Chee L.
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakov, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT APPLICATION NUMBER: US/09/385,328
; CURRENT FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 09/128,345
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
; LOCATION: 18
; NAME/KEY: SITE
; LOCATION: 6, 8, 13, 15
; OTHER INFORMATION: Xaa = hydrophobic, small or large polar amino acid
US-09-385-328-91

Query Match      71.4%; Score 65; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0008;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 RGRLSYSRRRPFSTGTGR 18
      ||||| | |||| | ||
DB      1 RGRGLXRRRFXVXVGR 18
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; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
US-09-385-328-91

Query Match      70.3%; Score 64; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 0.0012;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1 RGRLSYSRRRPFSTGTGR 18
      ||||| : |||| : ||
DB      1 RGRGLAWRRRFAVAVGR 18

RESULT 15
US-09-385-328-92
; Sequence 92, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Gu, Chee L.
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakov, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT APPLICATION NUMBER: US/09/385,328
; CURRENT FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 09/128,345
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
US-09-385-328-92

Query Match      70.3%; Score 64; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 0.0012;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1 RGRLSYSRRRPFSTGTGR 18
      ||||| : |||| : ||
DB      1 RGRGLAYARRRWAFAVGR 18

RESULT 16
US-08-499-523-53
; Sequence 53, Application US/08499523
; Patent No. 5804558
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
```

```

; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/499,523
; FILING DATE: 07-JUL-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 8..13
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: group(6, 15)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
; US-08-499-523-53

Query Match 69.2%; Score 63; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLYSRRRFFSTGSR 18
   ||||| |||||
Db 1 RGGRLXCRRRFFCVXGR 18

RESULT 17
US-08-499-523-58
; Sequence 58, Application US/08499523
; Patent No. 5804558
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/499,523
; FILING DATE: 07-JUL-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959

```

```

; REFERENCE/DOCKET NUMBER: 2000-0540.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 6..15
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: group(8, 13)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
; US-08-499-523-58

Query Match 69.2%; Score 63; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLYSRRRFFSTGSR 18
   ||||| |||||
Db 1 RGGRLCYRRRFFXCVGR 18

RESULT 18
US-09-128-345-53
; Sequence 53, Application US/09128345
; Patent No. 6159936
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura, A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 8..13

```

```
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: Group(6, 15)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; US-09-128-345-53
; OTHER INFORMATION: small, or a large polar amino acid"

Query Match 69.2%; Score 63; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0017; 6; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTGTGR 18
    ||||| ||||| ||
Db 1 RGGRLXCRRRFFCVVGR 18

RESULT 19
US-09-128-345-58
; Sequence 58, Application US/09128345
; Patent No. 615936
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S. L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Cotuzzi, Laura, A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 6..15
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: group(8, 13)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; US-09-128-345-58
; OTHER INFORMATION: small, or a large polar amino acid"

Query Match 69.2%; Score 63; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0017; 6; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTGTGR 18
    ||||| ||||| ||
Db 1 RGGRLCYRRRFFXVCVR 18
```

```
RESULT 20
US-09-385-328-90
; Sequence 90, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Gu, Chee L.
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakov, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT APPLICATION NUMBER: US/09/385,328
; CURRENT FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 09/128,345
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
; US-09-385-328-90

Query Match 69.2%; Score 63; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0017; 4; Indels 0; Gaps 0;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTGTGR 18
    ||||| ||||| ||
Db 1 RGGRLAYCRRRFFCVAWGR 18

RESULT 21
US-09-385-328-101
; Sequence 101, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Gu, Chee L.
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakov, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT APPLICATION NUMBER: US/09/385,328
; CURRENT FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 09/128,345
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
```

```
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
; NAME/KEY: SITE
; LOCATION: 6, 15
; OTHER INFORMATION: Xaa = hydrophobic, small or large polar amino acid
; NAME/KEY: DISULFID
; LOCATION: (8)...(13)
US-09-385-328-101

Query Match          69.2%; Score 63; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGR 18
    ||||| |||||
Db 1 RGGRLXCYRRRRCVXVGR 18

RESULT 22
US-09-385-328-106
; Sequence 106, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Gu, Chee L.
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakov, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT FILING DATE: 1999-08-30
; PRIOR FILING DATE: US 09/128,345
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
; NAME/KEY: SITE
; LOCATION: 8, 13
; OTHER INFORMATION: Xaa = hydrophobic, small or large polar amino acid
; NAME/KEY: DISULFID
; LOCATION: (6)...(15)
US-09-385-328-106

Query Match          69.2%; Score 63; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGR 18
    ||||| |||||
Db 1 RGGRLXCYRRRRCVXVGR 18

RESULT 23
US-08-499-523-54
; Sequence 54, Application US/08499523
; Patent No. 5804558
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
```

```
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/499,523
; FILING DATE: 07-JUL-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 8..13
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: group(6, 15)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-54

Query Match          68.1%; Score 62; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0024;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGR 18
    ||||| |||||
Db 1 RGGRLXCYRRRRCVXVGR 18

RESULT 24
US-08-499-523-59
; Sequence 59, Application US/08499523
; Patent No. 5804558
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/499,523
;; FILING DATE: 07-JUL-1995
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MURASHIGE, KATE H.
;; REGISTRATION NUMBER: 29,959
;; REFERENCE/DOCKET NUMBER: 2000-0540.24
;; TELEPHONE: (202) 887-1500
;; TELEFAX: (202) 887-0763
;; TELEX: 90-4030
;; INFORMATION FOR SEQ ID NO: 59:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: Disulfide-bond
;; LOCATION: 6..15
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: group(8, 13)
;; OTHER INFORMATION: /note= "X is a hydrophobic, a
;; OTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-59

Query Match 68.1%; Score 62; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0024;
Matches 12; Conservative 0; Mismatches 6; Indels 0;

QY 1 RGGRLSYRRRSTGTGR 18
|||||
DB 1 RGGRLCYRRRFXICVGR 18

RESULT 25
US-09-128-345-54
; Sequence 54, Application US/09128345
; Patent No. 6159936
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KORYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura, A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELEPHONE: (212) 790-9090
; TELEFAX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 6..15
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: group(8, 13)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"

;;
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: Disulfide-bond
;; LOCATION: 8..13
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: group(6, 15)
;; OTHER INFORMATION: /note= "X is a hydrophobic, a
;; OTHER INFORMATION: small, or a large polar amino acid"
US-09-128-345-54

Query Match 68.1%; Score 62; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0024;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRSTGTGR 18
|||||
DB 1 RGGRLCYRRRFXICVGR 18

RESULT 26
US-09-128-345-59
; Sequence 59, Application US/09128345
; Patent No. 6159936
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KORYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura, A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 6..15
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: group(8, 13)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"

US-09-128-345-59

Query Match 68.1%; Score 62; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0024;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRPFSTGTGR 18
||||| ||||| ||
Db 1 RGGRLCYRRRPFICVGR 18

RESULT 27

US-09-385-328-102
; Sequence 102, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Gu, Chee L.
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakov, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT APPLICATION NUMBER: US/09/385,328
; CURRENT FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 09/128,345
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
; NAME/KEY: SITE
; LOCATION: 6, 15
; OTHER INFORMATION: Xaa = hydrophobic, small or large polar amino acid
; NAME/KEY: DISULFID
; LOCATION: (8)...(13)
US-09-385-328-102

Query Match 68.1%; Score 62; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0024;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRPFSTGTGR 18
||||| ||||| ||
Db 1 RGGRLCYRRRPFICVGR 18

RESULT 28

US-09-385-328-107
; Sequence 107, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Gu, Chee L.
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakov, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT APPLICATION NUMBER: US/09/385,328
; CURRENT FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 09/128,345

; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
; NAME/KEY: SITE
; LOCATION: 8, 13
; OTHER INFORMATION: Xaa = hydrophobic, small or large polar amino acid
; NAME/KEY: DISULFID
; LOCATION: (6)...(15)
US-09-385-328-107

Query Match 68.1%; Score 62; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0024;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRPFSTGTGR 18
||||| ||||| ||
Db 1 RGGRLCYRRRPFICVGR 18

RESULT 29

US-08-095-769A-1
; Sequence 1, Application US/08095769A
; Patent No. 5464823
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; APPLICANT: HARWIG, SYLVIA S. L.
; TITLE OF INVENTION: NOVEL MAMMALIAN ANTIBIOTIC PEPTIDES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington, DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/095,769A
; FILING DATE: 26-JUL-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 220002054020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-095-769A-1

Query Match 67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;

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Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGRGLSYRRRSTSTGR 18
    ||||| ||||| ||
Db 1 RGRGLCYRRRRCVCVGR 18
    ||||| ||||| ||

RESULT 30
US-08-182-483A-2
; Sequence 2, Application US/08182483A
; Patent No. 5693486
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; APPLICANT: HARWIG, SYLVIA S.L.
; TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,483A
; FILING DATE: 13-JAN-1994
; CLASSIFICATION: 435
; NAME: MURASHIGE, KATE H.
; REGISTRATION/DOCKET NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-182-483A-2

Query Match 67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGRGLSYRRRSTSTGR 18
    ||||| ||||| ||
Db 1 RGRGLCYRRRRCVCVGR 18
    ||||| ||||| ||

RESULT 31
US-08-182-483A-28
; Sequence 28, Application US/08182483A
; Patent No. 5693486
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; APPLICANT: HARWIG, SYLVIA S.L.
; TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,879A
; FILING DATE: 17-MAY-1994
; CLASSIFICATION: 530
; NAME: MURASHIGE, KATE H.
; REGISTRATION/DOCKET NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-182-483A-28

Query Match 67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGRGLSYRRRSTSTGR 18
    ||||| ||||| ||
Db 1 RGRGLCYRRRRCVCVGR 18
    ||||| ||||| ||

RESULT 32
US-08-243-879A-1
; Sequence 1, Application US/08243879A
; Patent No. 5708145
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; TITLE OF INVENTION: A NEW PROTEGRIN
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington, DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,879A
; FILING DATE: 17-MAY-1994
; CLASSIFICATION: 530
; NAME: MURASHIGE, KATE H.
; REGISTRATION/DOCKET NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-243-879A-1

Query Match 67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RGRGLSYRRRSTSTGR 18
    ||||| ||||| ||
Db 1 RGRGLCYRRRRCVCVGR 18
    ||||| ||||| ||

RESULT 33
US-08-243-879A-1
; Sequence 1, Application US/08243879A
; Patent No. 5708145
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; TITLE OF INVENTION: A NEW PROTEGRIN
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington, DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,879A
; FILING DATE: 17-MAY-1994
; CLASSIFICATION: 530
; NAME: MURASHIGE, KATE H.
; REGISTRATION/DOCKET NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-243-879A-1
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; TOPOLOGY: linear
US-08-243-879A-1
Query Match 67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGTGR 18
    ||||| ||||| ||
Db 1 RGGRLCYRRRRFCVGVGR 18
    ||||| ||||| ||

RESULT 33
US-08-243-879A-27
; Sequence 27, Application US/08243879A
; Patent No. 5708145
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; TITLE OF INVENTION: A NEW PROTEGRIN
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington, DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243.879A
; FILING DATE: 17-MAY-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-243-879A-27

Query Match 67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRPFSTGTGR 18
    ||||| ||||| ||
Db 1 RATRISFRRRPFVSVGR 18
    ||||| ||||| ||

RESULT 34
US-08-499-523-11
; Sequence 11, Application US/08499523
; Patent No. 5804558
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KORYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/499,523
; FILING DATE: 07-JUL-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.

```

REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-499-523-16

Query Match 67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGRGLSYRRRFFSTGTGR 18
||||| | | | | | | |
DB 1 RGRGLCYCRRRCVCVGR 18

RESULT 36
US-08-499-523-33
Sequence 33, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Region
LOCATION: 1..18
OTHER INFORMATION: /note= "All D-form amino acids"

US-08-499-523-33
Query Match 67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGRGLSYRRRFFSTGTGR 18
||||| | | | | | | |
DB 1 RGRGLCYCRRRCVCVGR 18

QY 1 RGRGLSYRRRFFSTGTGR 18
||||| | | | | | | |
DB 1 RGRGLCYCRRRCVCVGR 18

RESULT 37
US-08-499-523-48
Sequence 48, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-499-523-48

Query Match 67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RGRGLSYRRRFFSTGTGR 18
||||| | | | | | | |
DB 1 RGRGLCYCRRRCVCVGR 18

RESULT 38
US-08-752-852A-1
Sequence 1, Application US/08752852A
Patent No. 5994306
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Chee-Liang
APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York

US-08-752-852A-1
Query Match 67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-034-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-752-852A-1

Query Match 67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18
||||| ||||| ||
Db 1 RGGRLCYRRRFFCVCVGR 18

RESULT 39
US-08-752-852A-9
Sequence 9, Application US/08752852A
Patent No. 5994306
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Chee-liang
APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-034-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 14...15
OTHER INFORMATION: Xaa=N-methyl valine
US-08-752-852A-9

Query Match 67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18
||||| ||||| ||
Db 1 RGGRLCYRRRFFCVCVGR 18

RESULT 40
US-08-752-852A-123
Sequence 123, Application US/08752852A
Patent No. 5994306
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Chee-liang
APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-034-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids

```
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-752-852A-123
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```
Query Match      67.0%; Score 61; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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QY      1 RGRGLSYRRRPFSTSTGR 18
      ||||| ||||| ||
Db       1 RGRGLCYRRRRCVGVGR 18
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Search completed: May 21, 2006, 00:25:42
Job time : 52 secs
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ALIGNMENTS

RESULT 1
US-10-336-312-1
; Sequence 1, Application US/10336312
; Publication No. US20030186890A1
; GENERAL INFORMATION:
; APPLICANT: DRIN, GUILLAUME
; APPLICANT: GOMAR, JEROME
; APPLICANT: TEMSAMANI, JAMAL
; APPLICANT: REES, ANTHONY B.
; TITLE OF INVENTION: AMPHIPHATIC LINEAR PEPTIDES AND FORMULATIONS CONTAINING
; FILE REFERENCE: 1534-02
; CURRENT APPLICATION NUMBER: US/10/336,312
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: PCT/FR01/02129
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: FR 00/08633
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Peptide SynB1
US-10-336-312-1

Query Match 100.0%; Score 91; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRRFSTSTGR 18
DB 1 RGGRLSYRRRRFSTSTGR 18

RESULT 2
US-10-136-187-24
; Sequence 24, Application US/10136187
; Publication No. US20030203865A1
; GENERAL INFORMATION:
; APPLICANT: Harvie, Pierrot
; APPLICANT: Paul, Ralph
; APPLICANT: Cudmore, Sally
; APPLICANT: O'Mahony, Daniel J.
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; FILE REFERENCE: 226272005300
; CURRENT APPLICATION NUMBER: US/10/136,187
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/287,786
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-136-187-24

Query Match 100.0%; Score 91; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRRFSTSTGR 18

DB 1 RGGRLSYRRRRFSTSTGR 18

RESULT 3
US-10-144-549-17
; Sequence 17, Application US/10144549
; Publication No. US20030211590A1
; GENERAL INFORMATION:
; APPLICANT: Geneshuttle Biopharm, Inc.
; APPLICANT: Hwu, Paul L.
; TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR
; FILE REFERENCE: MHB 02-340
; CURRENT APPLICATION NUMBER: US/10/144,549
; CURRENT FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Membrane fusion sequence.
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Synthetic sequence from protegrins/procine leukocyte.
US-10-144-549-17

Query Match 100.0%; Score 91; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRRFSTSTGR 18
DB 1 RGGRLSYRRRRFSTSTGR 18

RESULT 4
US-10-185-593-3
; Sequence 3, Application US/10185593
; Publication No. US20030220474A1
; GENERAL INFORMATION:
; APPLICANT: PACIFIC CORPORATION
; TITLE OF INVENTION: Conjugate of biodegradable aliphatic polyester with Tat49-57
; FILE REFERENCE: 2002dp109
; CURRENT APPLICATION NUMBER: US/10/185,593
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide derived from SynB1 of protegrins
US-10-185-593-3

Query Match 100.0%; Score 91; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRRFSTSTGR 18
DB 1 RGGRLSYRRRRFSTSTGR 18

RESULT 5
US-10-270-010-10
; Sequence 10, Application US/10270010
; Publication No. US20040072340A1
; GENERAL INFORMATION:

```
; APPLICANT: Johnson, Mark Elliott
; APPLICANT: Hamilton Day, Fiona
; APPLICANT: Kaczorek, Michel
; APPLICANT: Tensamani, Jamal
; TITLE OF INVENTION: Use of peptide vectors to improve the immune response
; TITLE OF INVENTION: to antigens
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/270,010
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: EP 01402671.0
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Linear
; OTHER INFORMATION: derivative of a beta-stranded antibiotic peptide
US-10-270-010-10

Query Match          100.0%; Score 91; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTGCR 18
   |||||
Db 1 RGGRLSYRRRFFSTGCR 18

RESULT 6
US-10-850-873-24
; Sequence 24, Application US/10850873
; Publication No. US20050025821A1
; GENERAL INFORMATION:
; APPLICANT: Harvie, Pierrot
; APPLICANT: Paul, Ralph
; APPLICANT: Cudmore, Sally
; APPLICANT: O'Mahony, Daniel J.
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
; FILE REFERENCE: 226272005300
; CURRENT APPLICATION NUMBER: US/10/850,873
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/10/136,187
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/287,786
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-850-873-24

Query Match          100.0%; Score 91; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTGCR 18
   |||||
Db 1 RGGRLSYRRRFFSTGCR 18

RESULT 7
US-10-878-175B-36
; Sequence 36, Application US/10878175B
; Publication No. US20050153913A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Kosak, Kenneth M.
; TITLE OF INVENTION: Nucleic Acid Carrier Compositions and Methods for Their Synthesis
; FILE REFERENCE: Confirmation No. 5281
; CURRENT APPLICATION NUMBER: US/10/878,175B
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Table I Transduction Peptide
US-10-878-175B-36

Query Match          100.0%; Score 91; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTGCR 18
   |||||
Db 1 RGGRLSYRRRFFSTGCR 18

RESULT 8
US-10-923-112A-36
; Sequence 36, Application US/10923112A
; Publication No. US20060040879A1
; GENERAL INFORMATION:
; APPLICANT: Kosak, Kenneth M.
; TITLE OF INVENTION: Chloroquine Coupled Nucleic Acids and Methods for Their Synthesis
; FILE REFERENCE: Confirmation No. 3293
; CURRENT APPLICATION NUMBER: US/10/923,112A
; CURRENT FILING DATE: 2004-08-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Table I Transduction Peptide
US-10-923-112A-36

Query Match          100.0%; Score 91; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTGCR 18
   |||||
Db 1 RGGRLSYRRRFFSTGCR 18

RESULT 9
US-11-027-967-3
; Sequence 3, Application US/11027967
; Publication No. US20050112089A1
; GENERAL INFORMATION:
; APPLICANT: PACIFIC CORPORATION
; TITLE OF INVENTION: Conjugate of biodegradable aliphatic polyester with Tat49-57
; TITLE OF INVENTION: peptide or peptide chain containing Tat49-57 peptide, and
; TITLE OF INVENTION: nanoparticle manufactured using the same
; FILE REFERENCE: 2002dp109
; CURRENT APPLICATION NUMBER: US/11/027,967
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: US/10/185,593
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

; FEATURE:
; OTHER INFORMATION: peptide derived from SynB1 of protegrins
US-11-027-967-3

Query Match 100.0%; Score 91; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGLSYRRRFRSTSTGR 18
| | | | | | | | | | | | | | | | | |
DB 1 RGRGLSYRRRFRSTSTGR 18

RESULT 10
US-10-270-010-7
; Sequence 7, Application US/10270010
; Publication No. US20040072340A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Mark Elliott
; APPLICANT: Hamilton Day, Piona
; APPLICANT: Kaczorek, Michel
; APPLICANT: Temsamani, Jamal
; TITLE OF INVENTION: Use of peptide vectors to improve the immune response
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/270,010
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: EP 01402671.0
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Linear
; OTHER INFORMATION: derivative of a beta-stranded antibiotic peptide
US-10-270-010-7

Query Match 89.0%; Score 81; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 8.3e-06;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGRGLSYRRRFRSTSTGR 18
| | | | | | | | | | | | | | | | | |
DB 1 RGRGLSYRRRFRFSVGR 18

RESULT 11
US-10-500-671A-15
; Sequence 15, Application US/10500671A
; Publication No. US20050170348A1
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Nuclear-Envelope and Nuclear-Lamina Binding Chimeras for
; FILE REFERENCE: 109845-163
; CURRENT APPLICATION NUMBER: US/10/500,671A
; CURRENT FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide Syn B1 from Antennapedia homeodomain protein
US-10-500-671A-15

Query Match 87.9%; Score 80; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGLSYRRRFRSTST 16
| | | | | | | | | | | | | | | | | |
DB 1 RGRGLSYRRRFRSTST 16

RESULT 12
US-09-810-601-42
; Sequence 42, Application US/09810601
; Patent No. US20020177545A1
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Compositions and Methods for Treating Gonadotrophin
; FILE REFERENCE: 2947
; CURRENT APPLICATION NUMBER: US/09/810,601
; CURRENT FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Membrane
; OTHER INFORMATION: Translocation Peptide
; PUBLICATION INFORMATION:
; AUTHORS: Rousselle, Christophe
; JOURNAL: Mol. Pharmacol.
; VOLUME: 57
; PAGES: 679-686
; DATE: 2000
US-09-810-601-42

Query Match 87.9%; Score 80; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.2e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGRGLSYRRRFRSTSTGR 18
| | | | | | | | | | | | | | | | | |
DB 1 RGRKSWRRRFRSTSTGR 18

RESULT 13
US-10-336-312-26
; Sequence 26, Application US/10336312
; Publication No. US20030186890A1
; GENERAL INFORMATION:
; APPLICANT: DRIN, GUILLAUME
; APPLICANT: GOMAR, JEROME
; APPLICANT: TEMSAMANI, JAMAL
; APPLICANT: REES, ANTHONY B.
; TITLE OF INVENTION: AMPHIPATHIC LINEAR PEPTIDES AND FORMULATIONS CONTAINING
; FILE REFERENCE: 1534-02
; CURRENT APPLICATION NUMBER: US/10/336,312
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: PCT/FR01/02129
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: FR 00/08633
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide SynB/2c1t
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)..(10)


```
; OTHER INFORMATION: Citrulline
US-10-336-312-26
Query Match      86.8%; Score 79; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRRFSTSTGR 18
    |||||
Db 1 RGGRLSYRRRRFSTSTGR 18
    |||||

RESULT 14
US-10-336-312-27
; Sequence 27, Application US/10336312
; Publication No. US20030186890A1
; GENERAL INFORMATION:
; APPLICANT: DRIN, GUILLAUME
; APPLICANT: GOMAR, JEROME
; APPLICANT: TEMSAMANI, JAMAL
; TITLE OF INVENTION: AMPHIPATHIC LINEAR PEPTIDES AND FORMULATIONS CONTAINING
; FILE REFERENCE: 1534-02
; CURRENT APPLICATION NUMBER: US/10/336,312
; PRIOR FILING DATE: 2003-02-27
; PRIOR FILING DATE: 2001-07-03
; PRIOR FILING DATE: 2001-07-03
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide SynBl/3cit
; NAME/KEY: MOD RES
; LOCATION: (9)..(11)
; OTHER INFORMATION: Citrulline
US-10-336-312-27

Query Match      80.2%; Score 73; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.00016;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRRFSTSTGR 18
    |||||
Db 1 RGGRLSYRRRRFSTSTGR 18
    |||||

RESULT 16
US-10-336-312-7
; Sequence 7, Application US/10336312
; Publication No. US20030186890A1
; GENERAL INFORMATION:
; APPLICANT: DRIN, GUILLAUME
; APPLICANT: GOMAR, JEROME
; APPLICANT: TEMSAMANI, JAMAL
; TITLE OF INVENTION: AMPHIPATHIC LINEAR PEPTIDES AND FORMULATIONS CONTAINING
; FILE REFERENCE: 1534-02
; CURRENT APPLICATION NUMBER: US/10/336,312
; CURRENT FILING DATE: 2003-02-27
; PRIOR FILING DATE: PCT/FR01/02129
; PRIOR FILING DATE: 2001-07-03
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide PG-4A
US-10-336-312-7

Query Match      75.8%; Score 69; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.00067;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRRFSTSTGR 18
    |||||
Db 1 RGGRLSYRRRRFSTSTGR 18
    |||||

RESULT 17
US-09-539-443-63
; Sequence 63, Application US/09539443
; Publication No. US20030100483A1
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
```

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/539,443
FILING DATE: 30-MARCH-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
NAME/KEY: Modified-site
LOCATION: group(6, 8, 13, 15)
OTHER INFORMATION: /note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
US-09-539-443-63

Query Match 71.4%; Score 65; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0029;
Matches 12; Conservative 0; Mismatches 6; Indels 0;

QY 1 RGGRLSYRRRFRSTGTGR 18
Db 1 RGGRLXXRRRFXVXVGR 18

RESULT 18
US-09-539-443-67
Sequence 67, Application US/09539443
Publication No. US20030100483A1
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/539,443
FILING DATE: 30-MARCH-2000
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: group(6, 8, 13, 15)
OTHER INFORMATION: /note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
US-09-539-443-67

Query Match 71.4%; Score 65; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0029;
Matches 12; Conservative 0; Mismatches 6; Indels 0;

QY 1 RGGRLSYRRRFRSTGTGR 18
Db 1 RGGRLXXRRRFXVXVGR 18

RESULT 19
US-10-627-829-63
Sequence 63, Application US/10627829
Publication No. US20040152638A1
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,829
FILING DATE: 24-JULY-2003
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/539,443
FILING DATE: 30-MARCH-2000
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 63:

SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: group(6, 8, 13, 15)
OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
US-10-627-829-63

Query Match 71.4%; Score 65; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0029;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18
Db 1 RGGRLXYRRRFXVXVGR 18

RESULT 20

US-10-627-829-67
; Sequence 67, Application US/10627829
; Publication No. US20040152638A1
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,829
; FILING DATE: 24-JULY-2003

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/539,443
FILING DATE: 30-MARCH-2000
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: Modified-site
LOCATION: group(6, 8, 13, 15)
OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
US-10-627-829-67

Query Match 71.4%; Score 65; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0029;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18
Db 1 RGGRLXYRRRFXVXVGR 18

RESULT 21

US-09-539-443-53
; Sequence 53, Application US/09539443
; Publication No. US20030100483A1
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/539,443
; FILING DATE: 30-MARCH-2000
; CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 8..13
FEATURE:
NAME/KEY: Modified-site
LOCATION: group(6, 15)
OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
US-09-539-443-53

Query Match 69.2%; Score 63; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0061;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18
Db 1 RGGRLXYRRRFXVXVGR 18

RESULT 22

US-09-539-443-58

; Sequence 58, Application US/09539443
; Publication No. US20030100483A1
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/539,443
; FILING DATE: 30-MARCH-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura, A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 6..15
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: group(8, 13)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
; US-09-539-443-58

Query Match 69.2%; Score 63; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0061;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRSTSTGR 18
||| | | | | |
DB 1 RGGRLCYRRRFXCVGR 18

RESULT 23
US-10-627-829-53
; Sequence 53, Application US/10627829
; Publication No. US20040152638A1
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas

; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,829
; FILING DATE: 24-JULY-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/539,443
; FILING DATE: 30-MARCH-2000
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura, A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 8..13
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: group(6, 15)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
; US-10-627-829-53

Query Match 69.2%; Score 63; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0061;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRSTSTGR 18
||| | | | | |
DB 1 RGGRLCYRRRFXCVGR 18

RESULT 24
US-10-627-829-58
; Sequence 58, Application US/10627829
; Publication No. US20040152638A1
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,829
; FILING DATE: 24-JULY-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/539,443
; FILING DATE: 30-MARCH-2000
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura, A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; NAME/KEY: Disulfide-bond
; LOCATION: 6..15
; FEATURE:
; NAME/KEY: Modified-eite
; LOCATION: group(8, 13)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
;
US-10-627-829-58

```

```

Query Match 69.2%; Score 63; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0061;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy 1 RGRLSYRRRPFSTGCR 18
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Db 1 RGRLCYRRRFXVCVGR 18

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RESULT 25
US-09-539-443-54
; Sequence 54, Application US/09539443
; Publication No. US20030100483A1
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARMIG, SYLVIA S.L.
; APPLICANT: KORYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/539,443
; FILING DATE: 30-MARCH-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura, A.

```

```

; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 8..13
; FEATURE:
; NAME/KEY: Modified-eite
; LOCATION: group(6, 15)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
;
US-09-539-443-54

```

```

Query Match 68.1%; Score 62; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0086;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

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Qy 1 RGRLSYRRRPFSTGCR 18
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Db 1 RGRLCYRRRFXVCVGR 18

```

```

RESULT 26
US-09-539-443-59
; Sequence 59, Application US/09539443
; Publication No. US20030100483A1
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARMIG, SYLVIA S.L.
; APPLICANT: KORYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/539,443
; FILING DATE: 30-MARCH-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura, A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

```

; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 6..15
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: group(8, 13)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
US-09-539-443-59

Query Match 68.1%; Score 62; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0088;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGRGLSYRRRFRSTSTGR 18
|||||
Db 1 RGRGLCYXRRRFXICVGR 18

RESULT 27
US-10-627-829-54
; Sequence 54, Application US/10627829
; Publication No. US20040152638A1
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,829
; FILING DATE: 24-JULY-2003

CLASSIFICATION:
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/539,443
; FILING DATE: 30-MARCH-2000
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura, A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 8..13
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: group(6, 15)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"

US-10-627-829-54
Query Match 68.1%; Score 62; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0088;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGRGLSYRRRFRSTSTGR 18
|||||
Db 1 RGRGLCYXRRRFXICVGR 18

RESULT 28
US-10-627-829-59
; Sequence 59, Application US/10627829
; Publication No. US20040152638A1
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,829
; FILING DATE: 24-JULY-2003
; CLASSIFICATION:
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/539,443
; FILING DATE: 30-MARCH-2000
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura, A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 6..15
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: group(8, 13)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
US-10-627-829-59

Query Match 68.1%; Score 62; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0088;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGRGLSYRRRFRSTSTGR 18
|||||
Db 1 RGRGLCYXRRRFXICVGR 18

RESULT 29

US-09-030-619-221
; Sequence 221, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; FILE REFERENCE: 660081.406
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 221
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Sus scrofa

US-09-030-619-221

Query Match 67.0%; Score 61; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.013;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTSTGR 18
||||| ||||| ||
Db 1 RGGRLCYRRRFFCVGVR 18

RESULT 30

US-09-912-609-109
; Sequence 109, Application US/09912609
; Publication No. US20020041898A1
; GENERAL INFORMATION:
; APPLICANT: UNGER, EVAN C.
; APPLICANT: MATSUNAGA, TERRY ONICHI
; APPLICANT: RAMASWAMI, VARADARAJAN
; APPLICANT: ROMANOWSKI, MAREK J.
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 5030-0001.24
; CURRENT APPLICATION NUMBER: US/09/912,609
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 09/703,474
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 09/478,124
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide

US-09-912-609-109

Query Match 67.0%; Score 61; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.013;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTSTGR 18
||||| ||||| ||
Db 1 RGGRLCYRRRFFCVGVR 18

RESULT 31

US-09-539-443-11
; Sequence 11, Application US/09539443
; Publication No. US20030100483A1
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KORYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/539,443
; FILING DATE: 30-MARCH-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura, A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 4..13
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 6..11
; US-09-539-443-11

Query Match 67.0%; Score 61; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.013;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTSTGR 18
||||| ||||| ||
Db 1 RGGRLCYRRRFFCVGVR 18

RESULT 32

US-09-539-443-16
; Sequence 16, Application US/09539443
; Publication No. US20030100483A1
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; APPLICANT: KORYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/539,443
FILING DATE: 30-MARCH-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-539-443-16

Query Match 67.0%; Score 61; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.013;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGRLSYSRRRSTSTGR 18
Db 1 RGRLCYCRRRFCVCVGR 18

RESULT 33
US-09-539-443-33
Sequence 33, Application US/09539443
Publication No. US20030100483A1
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/539,443
FILING DATE: 30-MARCH-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura, A.
REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Region
LOCATION: 1..18
OTHER INFORMATION: /note= "All D-form amino acids"
US-09-539-443-33
Query Match 67.0%; Score 61; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.013;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 RGRLSYSRRRSTSTGR 18
Db 1 RGRLCYCRRRFCVCVGR 18
RESULT 34
US-09-539-443-48
Sequence 48, Application US/09539443
Publication No. US20030100483A1
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/539,443
FILING DATE: 30-MARCH-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-539-443-48
Query Match 67.0%; Score 61; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.013;

Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTSTGR 18
| : ||||| ||
Db 1 RATRISFRRRFFSVSVGR 18

RESULT 35

US-10-077-624-15
; Sequence 15, Application US/10077624
; Publication No. US20030143234A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: WASHINGTON DENTAL SERVICE
; APPLICANT: Shi, Wenyuan
; APPLICANT: Anderson, Maxwell
; APPLICANT: Morrison, Sherie
; APPLICANT: Trinh, Kham
; APPLICANT: Wims, Letitia
; APPLICANT: Chen, Li
; APPLICANT: Qi, Fengxia
; TITLE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL
; FILE REFERENCE: 2101363-991200
; CURRENT APPLICATION NUMBER: US/10/077,624
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 09/910,358
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Protegrin PG-1
US-10-077-624-15

Query Match 67.0%; Score 61; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.013;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTSTGR 18
| : ||||| ||
Db 1 RGGRLCYRRRFFCVCVGR 18

RESULT 36

US-10-313-994-11
; Sequence 11, Application US/10313994
; Publication No. US20030162718A1
; GENERAL INFORMATION:
; APPLICANT: Selssted, Michael E.
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Yuan, Jun
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
; FILE REFERENCE: P-UC 3095
; CURRENT APPLICATION NUMBER: US/10/313,994
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: US/09/309,487
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-313-994-11

Query Match 67.0%; Score 61; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.013;

Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTSTGR 18
| : ||||| ||
Db 1 RGGRLCYRRRFFCVCVGR 18

RESULT 37

US-10-277-232-221
; Sequence 221, Application US/10277232
; Publication No. US20030211537A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Efile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; FILE REFERENCE: 660081.406C1
; CURRENT APPLICATION NUMBER: US/10/277,232
; CURRENT FILING DATE: 2002-11-27
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 221
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-277-232-221

Query Match 67.0%; Score 61; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.013;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTSTGR 18
| : ||||| ||
Db 1 RGGRLCYRRRFFCVCVGR 18

RESULT 38

US-10-277-233-221
; Sequence 221, Application US/10277233
; Publication No. US20030232750A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Efile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; FILE REFERENCE: 660081.406C1
; CURRENT APPLICATION NUMBER: US/10/277,233
; CURRENT FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 221
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-277-233-221

Query Match 67.0%; Score 61; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.013;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGGRLSYRRRFFSTSTGR 18
| : ||||| ||
Db 1 RGGRLCYRRRFFCVCVGR 18

Job time : 182 secs

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RESULT 39
US-10-427-715-32
; Sequence 32, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tran, Dat Q.
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; TITLE OF INVENTION: Thereof, and Methods of Use
; FILE REFERENCE: 66778-302(UC5754)
; CURRENT APPLICATION NUMBER: US/10/427,715
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/377,071
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: at the C terminus
US-10-427-715-32

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```

Query Match      67.0%; Score 61; DB 4; Length 18;
Best Local Similarity 66.7%; Pred.No. 0.013;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 RGGRLSYRRRPFSTGTR 18
        ||||| ||||| ||
Db       1 RGGRLCYCRRRPFVCVGR 18

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```

RESULT 40
US-10-427-715-33
; Sequence 33, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tran, Dat Q.
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; TITLE OF INVENTION: Thereof, and Methods of Use
; FILE REFERENCE: 66778-302(UC5754)
; CURRENT APPLICATION NUMBER: US/10/427,715
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/377,071
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-427-715-33

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Query Match      67.0%; Score 61; DB 4; Length 18;
Best Local Similarity 66.7%; Pred.No. 0.013;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 RGGRLSYRRRPFSTGTR 18
        ||||| ||||| ||
Db       1 RGGRLCYCRRRPFVCVGR 18

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Search completed: May 21, 2006, 00:39:20

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 21, 2006, 00:36:21 ; Search time 9 Seconds
(without alignments)
4.272 Million cell updates/sec

Title: US-09-857-000a-11

Perfect score: 91

Sequence: 1 RGRLSYRRRPFSTSTGR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pbp.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pbp.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pbp.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pbp.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pbp.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pbp.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pbp.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	40.7	413	7	US-11-249-111-87
2	34.5	37.9	390	7	US-11-242-505A-27
3	34	37.4	421	6	US-10-505-928-410
4	34	37.4	967	6	US-10-505-928-795
5	33.5	36.8	4059	6	US-10-501-834-6
6	33	36.3	525	6	US-10-196-749-436
7	32	35.2	95	7	US-11-239-308-40
8	32	35.2	226	6	US-10-505-928-193
9	32	35.2	302	7	US-11-058-746-9
10	32	35.2	352	7	US-11-242-505A-6
11	32	35.2	362	6	US-10-511-937-2509
12	32	35.2	372	7	US-11-058-746-10
13	32	35.2	383	7	US-11-058-746-6
14	32	35.2	384	7	US-11-058-746-7
15	32	35.2	640	7	US-11-249-111-96
16	32	35.2	3256	6	US-10-505-928-357
17	31	34.1	180	6	US-10-505-928-648
18	31	34.1	235	7	US-11-266-747-434
19	31	34.1	551	7	US-11-264-784-34
20	31	34.1	708	6	US-10-505-928-416
21	31	34.1	747	7	US-11-261-384-2
22	31	34.1	901	6	US-10-511-455-52
23	31	34.1	938	6	US-10-511-455-54
24	31	34.1	950	6	US-10-511-937-2603
25	31	34.1	1924	6	US-10-512-386-56

Sequence 7, Appli
Sequence 3, Appli
Sequence 131, App
Sequence 132, App
Sequence 133, App
Sequence 175, App
Sequence 176, App
Sequence 177, App
Sequence 178, App
Sequence 179, App
Sequence 24, Appl
Sequence 16, Appl
Sequence 2, Appli
Sequence 2466, Ap
Sequence 2608, Ap
Sequence 2530, Ap
Sequence 845, App
Sequence 6, Appli
Sequence 389, App
Sequence 6, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2421, Ap
Sequence 13, Appl
Sequence 7, Appli
Sequence 17, Appl
Sequence 171, App
Sequence 124, App
Sequence 125, App
Sequence 173, App
Sequence 2, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 10, Appl
Sequence 12, Appl
Sequence 121, App
Sequence 122, App
Sequence 123, App
Sequence 126, App
Sequence 127, App
Sequence 167, App
Sequence 168, App
Sequence 169, App
Sequence 170, App
Sequence 172, App
Sequence 784, App
Sequence 1, Appli
Sequence 8, Appli
Sequence 12, Appl
Sequence 57, Appl
Sequence 2549, Ap
Sequence 514, App
Sequence 457, App
Sequence 757, App
Sequence 14, Appl
Sequence 154, App
Sequence 3, Appli
Sequence 3007, Ap
Sequence 364, App
Sequence 43, Appl
Sequence 769, App
Sequence 770, App
Sequence 772, App
Sequence 636, App
Sequence 436, App
Sequence 536, App
Sequence 2469, Ap
Sequence 67, Appl
Sequence 70, Appl
Sequence 2, Appli
Sequence 4, Appli
Sequence 33, Appl

99 28 30.8 653 7 US-11-183-218-66 Sequence 66, Appl
100 28 30.8 694 6 US-10-505-928-312 Sequence 312, App

ALIGNMENTS

RESULT 1
US-11-249-111-87
; Sequence 87, Application US/11249111
; Publication No. US20060099623A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Lubbers, Mark W
; APPLICANT: Dekker, James
; TITLE OF INVENTION: Polynucleotides and polypeptides isolated from Lactobacillus
; FILE OF INVENTION: and methods for their use.
; FILE REFERENCE: 13353.1048ulc2
; CURRENT APPLICATION NUMBER: US/11/249,111
; CURRENT FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: 10/288,930
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/724,623
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/148,801
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-11-249-111-87

Query Match 40.7%; Score 37; DB 7; Length 413;
Best Local Similarity 42.9%; Pred. No. 7.2;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 5 LSYRRRFFSTGTGR 18
||| | : : :
Db 88 LSYKRRKITTAVGK 101

RESULT 2
US-11-242-505A-27
; Sequence 27, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; FILE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; FILE REFERENCE: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-242-505A-27

Query Match 37.9%; Score 34.5; DB 7; Length 390;

Best Local Similarity 71.4%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3 GRLSYRRRFFSTGT 16
||| | : : :
Db 230 GRLS-SRRSLAST 242

RESULT 3
US-10-505-928-410
; Sequence 410, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 410
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-410

Query Match 37.4%; Score 34; DB 6; Length 421;
Best Local Similarity 40.0%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 RLSYSRRRFFSTGTGR 18
| : | | | : : |
Db 334 RMSYQRAWEVDGR 348

RESULT 4
US-10-505-928-795
; Sequence 795, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 795
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-795

Query Match 37.4%; Score 34; DB 6; Length 967;
Best Local Similarity 47.4%; Pred. No. 69;
Matches 9; Conservative 1; Mismatches 3; Indels 6; Gaps 1;

QY 2 GGRLSYSR-----RRFST 14
||| | : : |
Db 893 GGSFSSNLIQAVTRRST 911

RESULT 5
US-10-501-834-6
; Sequence 6, Application US/10501834
; Publication No. US20060088628A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Peter C., Ward, Christopher J., Rossetti, Sandro, and Torres,
; APPLICANT: Vicente E.

; TITLE OF INVENTION: Polycystic Kidney Disease Nucleic Acids
; FILE REFERENCE: 07039/386US1
; CURRENT APPLICATION NUMBER: US/10/501,834
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: PCT/US03/02038
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 60/351,110
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 4059
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 2511
; OTHER INFORMATION: Xaa = Pro or Ser
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 2981
; OTHER INFORMATION: Arg or Gln
US-10-501-834-6

Query Match 36.8%; Score 33.5; DB 6; Length 4059;
Best Local Similarity 62.5%; Pred. No. 4.4e+02;
Matches 10; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

Qy 6 SYSTRRPFSTSTG 18
||| ||||| |||||
Db 2266 SYLDGRFSTSTVGR 2281

RESULT 6
US-10-196-749-436
; Sequence 436, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 436
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-196-749-436

Query Match 36.3%; Score 33; DB 6; Length 525;
Best Local Similarity 57.1%; Pred. No. 52;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGRLSYRRRPFSTG 15
||| ||||| |||||
Db 50 GGGASYSLRRCLSS 63

RESULT 7
US-11-239-308-40
; Sequence 40, Application US/11239308
; Publication No. US2006008883A1
; GENERAL INFORMATION:
; APPLICANT: Smider, Vaughn
; APPLICANT: Larrick, James W.
; APPLICANT: Integrigen, Inc.
; TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
; FILE REFERENCE: 021216-000310US
; CURRENT APPLICATION NUMBER: US/11/239,308
; CURRENT FILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US/10/683,733
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/417,979
; PRIOR FILING DATE: 2002-10-09
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-239-308-40

Query Match 35.2%; Score 32; DB 7; Length 95;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 4 RLSYSRRRPFSTG 17
|::| |||||
Db 3 RMTQSPFSFSAATG 16

RESULT 8
US-10-505-928-193
; Sequence 193, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 193
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-193

Query Match 35.2%; Score 32; DB 6; Length 226;

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Best Local Similarity 44.4%; Pred. No. 30;
Matches 8; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 1 RGGRLSYRRRFFSTSTG 18
    ||| :|:| | :||
Db 180 RGGPIRFS-----SSRSOR 193

RESULT 9
US-11-058-746-9
; Sequence 9, Application US/11058746
; Publication No. US20060101543A1
; GENERAL INFORMATION:
; APPLICANT: Somerville, Chris
; APPLICANT: Broun, Pierre
; APPLICANT: Van de Loo, Frank
; APPLICANT: Boddupalli, Sekhar S
; TITLE OF INVENTION: PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY MODIFIED
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 56100-5022-12
; CURRENT APPLICATION NUMBER: US/11/058,746
; CURRENT FILING DATE: 2005-02-16
; PRIOR APPLICATION NUMBER: US 08/597,313
; PRIOR FILING DATE: 1996-02-06
; PRIOR APPLICATION NUMBER: US 08/530,862
; PRIOR FILING DATE: 1995-09-20
; PRIOR APPLICATION NUMBER: US 08/320,982
; PRIOR FILING DATE: 1994-10-11
; PRIOR APPLICATION NUMBER: US 08/314,596
; PRIOR FILING DATE: 1994-09-26
; PRIOR APPLICATION NUMBER: PCT/US95/11855
; PRIOR FILING DATE: 1995-09-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Glycine max
US-11-058-746-9

Query Match 35.2%; Score 32; DB 7; Length 302;
Best Local Similarity 54.5%; Pred. No. 42;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 YSRRRFFSTSTG 17
    ||| ||| :|:|
Db 80 YSHRRHHSNTG 90

RESULT 10
US-11-242-505A-6
; Sequence 6, Application US/11242505A
; Publication No. US2006099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19311
; FILE REFERENCE: MFI2001-288P1RCP10NM1M
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6

```

; PRIOR APPLICATION NUMBER: US 08/320,982
; PRIOR FILING DATE: 1994-10-11
; PRIOR APPLICATION NUMBER: US 08/314,596
; PRIOR FILING DATE: 1994-09-26
; PRIOR APPLICATION NUMBER: PCT/US95/11855
; PRIOR FILING DATE: 1995-09-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (372)..(372)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-058-746-10

Query Match 35.2%; Score 32; DB 7; Length 372;
Best Local Similarity 54.5%; Pred. No. 54;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 YSRRRFSTGT 17
||| :||
DB 129 YSHRRHSNTG 139

RESULT 13
US-11-058-746-6
; Sequence 6, Application US/11058746
; Publication No. US20060101543A1
; GENERAL INFORMATION:
; APPLICANT: Somerville, Chris
; APPLICANT: Broun, Pierre
; APPLICANT: Van de Loo, Frank
; APPLICANT: Boddupalli, Sekhar S
; TITLE OF INVENTION: PRODUCTION OF HYDROXYLATED PATTY ACIDS IN GENETICALLY MODIFIED
; FILE OF INVENTION: PLANTS
; FILE REFERENCE: 56100-5022-12
; CURRENT APPLICATION NUMBER: US/11/058,746
; PRIOR FILING DATE: 2005-02-16
; PRIOR APPLICATION NUMBER: US 08/597,313
; PRIOR FILING DATE: 1996-02-06
; PRIOR APPLICATION NUMBER: US 08/530,862
; PRIOR FILING DATE: 1995-09-20
; PRIOR APPLICATION NUMBER: US 08/320,982
; PRIOR FILING DATE: 1994-10-11
; PRIOR APPLICATION NUMBER: US 08/314,596
; PRIOR FILING DATE: 1994-09-26
; PRIOR APPLICATION NUMBER: PCT/US95/11855
; PRIOR FILING DATE: 1995-09-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-058-746-6

Query Match 35.2%; Score 32; DB 7; Length 383;
Best Local Similarity 54.5%; Pred. No. 56;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 YSRRRFSTGT 17
||| :||
DB 139 YSHRRHSNTG 149

RESULT 14
US-11-058-746-7
; Sequence 7, Application US/11058746
; Publication No. US20060101543A1
; GENERAL INFORMATION:

; APPLICANT: Somerville, Chris
; APPLICANT: Broun, Pierre
; APPLICANT: Van de Loo, Frank
; APPLICANT: Boddupalli, Sekhar S
; TITLE OF INVENTION: PRODUCTION OF HYDROXYLATED PATTY ACIDS IN GENETICALLY MODIFIED
; FILE OF INVENTION: PLANTS
; FILE REFERENCE: 56100-5022-12
; CURRENT APPLICATION NUMBER: US/11/058,746
; PRIOR FILING DATE: 2005-02-16
; PRIOR APPLICATION NUMBER: US 08/597,313
; PRIOR FILING DATE: 1996-02-06
; PRIOR APPLICATION NUMBER: US 08/530,862
; PRIOR FILING DATE: 1995-09-20
; PRIOR APPLICATION NUMBER: US 08/320,982
; PRIOR FILING DATE: 1994-10-11
; PRIOR APPLICATION NUMBER: US 08/314,596
; PRIOR FILING DATE: 1994-09-26
; PRIOR APPLICATION NUMBER: PCT/US95/11855
; PRIOR FILING DATE: 1995-09-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (384)..(384)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-058-746-7

Query Match 35.2%; Score 32; DB 7; Length 384;
Best Local Similarity 54.5%; Pred. No. 56;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 YSRRRFSTGT 17
||| :||
DB 139 YSHRRHSNTG 149

RESULT 15
US-11-249-111-96
; Sequence 96, Application US/11249111
; Publication No. US20060099623A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Lubbers, Mark W
; APPLICANT: Dekker, James
; TITLE OF INVENTION: Polynucleotides and polypeptides isolated from Lactobacillus
; FILE OF INVENTION: and methods for their use.
; FILE REFERENCE: 13353.1048u1c2
; CURRENT APPLICATION NUMBER: US/11/249,111
; PRIOR FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: 10/288,930
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/724,623
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/148,801
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(640)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-249-111-96

Query Match 35.2%; Score 32; DB 7; Length 640;
Best Local Similarity 46.2%; Pred. No. 1e+02;

Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 RLSYSRRRSTST 16
:|:|:|:|:|:|
Db 201 QLGFKLRRFKTGT 213

RESULT 16

US-10-505-928-357
; Sequence 357, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 357
; LENGTH: 3256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-357

Query Match 35.2%; Score 32; DB 6; Length 3256;
Best Local Similarity 54.5%; Pred. No. 6.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 8 SRRRSTSTGR 18
:|:|:|:|:|:|
Db 1629 SKRLKTSLSGK 1639

RESULT 17

US-10-505-928-648
; Sequence 648, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 648
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-648

Query Match 34.1%; Score 31; DB 6; Length 180;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 SYSRRRSTSTG 17
:|:|:|:|:|:|
Db 34 SSSRRRRSCCTG 45

RESULT 18

US-11-266-747-434
; Sequence 434, Application US/11266747
; Publication No. US2006009700A1
; GENERAL INFORMATION:
; APPLICANT: Davis, S. Christopher
; APPLICANT: Fox, Richard J.
; APPLICANT: Gavrilovic, Vesna

; APPLICANT: Huisman, Gjalte W.
; APPLICANT: Mundorff, Emily C.
; APPLICANT: Newman, Lisa M.
; TITLE OF INVENTION: Improved Halohydrin Dehalogenases and Related Polynucleotides
; FILE REFERENCE: 16028US05 0353.510US
; CURRENT APPLICATION NUMBER: US/11/266,747
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 11/067,323
; PRIOR FILING DATE: 2005-02-23
; PRIOR APPLICATION NUMBER: 10/917,179
; PRIOR FILING DATE: 2004-08-11
; PRIOR APPLICATION NUMBER: 60/546,033
; PRIOR FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: 60/494,382
; PRIOR FILING DATE: 2003-08-11
; NUMBER OF SEQ ID NOS: 2848
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 434
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-266-747-434

Query Match 34.1%; Score 31; DB 7; Length 235;
Best Local Similarity 54.5%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GRLYSRRRFS 13
:|:|:|:|:|:|
Db 135 GALAYSTARFA 145

RESULT 19

US-11-264-784-34
; Sequence 34, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Magnaporthe grisea
US-11-264-784-34

Query Match 34.1%; Score 31; DB 7; Length 551;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 RGGRLYSRRRPFST 16
:|:|:|:|:|:|
Db 512 RGGQSLKVRNQRST 527

RESULT 20
US-10-505-928-416


```
; Sequence 416, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 416
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-416

Query Match      34.1%; Score 31; DB 6; Length 708;
Best Local Similarity 44.4%; Pred. No. 1.7e+02;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      1 RGGRLSYRRRFFSTGCR 18
      |||||
Db      577 RGGGQNSASRGSGQR 594
      |||||

RESULT 21
US-11-261-384-2
; Sequence 2, Application US/11261384
; Publication No. US20060095979A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CLCN4
; FILE REFERENCE: R-890
; CURRENT APPLICATION NUMBER: US/11/261,384
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/109,562
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/280,312
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 60/324,640
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 747
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-261-384-2

Query Match      34.1%; Score 31; DB 7; Length 747;
Best Local Similarity 42.9%; Pred. No. 1.8e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      5 LSYRRRFFSTGCR 18
      ::::|
Db      341 IAWCRRTKTLGR 354
      ::::|

RESULT 22
US-10-511-455-54
; Sequence 52, Application US/10511455
; Publication No. US20060088835A1
; GENERAL INFORMATION:
; APPLICANT: Pickard, Benjamin Simon
; APPLICANT: Blackwood, Douglas
; APPLICANT: Porteous, David
; APPLICANT: Muir, Walter John
; APPLICANT: Mors, Ole
; APPLICANT: Ewald, Henrik Lykke
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES
; FILE REFERENCE: 9013.63
; CURRENT APPLICATION NUMBER: US/10/511,455
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: PCT/GB03/001543
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: GB0207902.8
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207904.4
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207900.2
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207901.0
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0227734.1
; PRIOR FILING DATE: 2002-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 938
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-455-54

Query Match      34.1%; Score 31; DB 6; Length 938;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
```

```
; FILE REFERENCE: 9013.63
; CURRENT APPLICATION NUMBER: US/10/511,455
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: PCT/GB03/001543
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: GB0207902.8
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207904.4
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207900.2
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207901.0
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0227734.1
; PRIOR FILING DATE: 2002-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 901
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-455-52

Query Match      34.1%; Score 31; DB 6; Length 901;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY      1 RGGRLSYRRRFFSTST 16
      :|||
Db      576 KGG--SASRRRLSSAS 589
      :|||

RESULT 23
US-10-511-455-54
; Sequence 54, Application US/10511455
; Publication No. US20060088835A1
; GENERAL INFORMATION:
; APPLICANT: Pickard, Benjamin Simon
; APPLICANT: Blackwood, Douglas
; APPLICANT: Porteous, David
; APPLICANT: Muir, Walter John
; APPLICANT: Mors, Ole
; APPLICANT: Ewald, Henrik Lykke
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES
; FILE REFERENCE: 9013.63
; CURRENT APPLICATION NUMBER: US/10/511,455
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: PCT/GB03/001543
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: GB0207902.8
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207904.4
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207900.2
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0207901.0
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0227734.1
; PRIOR FILING DATE: 2002-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 938
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-455-54

Query Match      34.1%; Score 31; DB 6; Length 938;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
```

```
Db      613 KGG--SASRRRLSSAS 626

RESULT 24
US-10-511-937-2603
; Sequence 2603, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2603
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2603

Query Match      34.1%; Score 31; DB 6; Length 950;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 RGGRLSYSR 9
      |||||
Db      925 RGGGQGYPR 933

RESULT 25
US-10-512-386-56
; Sequence 56, Application US/10512386
; Publication No. US20060088837A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR STEM-LOOP RNA MOLECULES HAVING RNAI EFFECT
; FILE REFERENCE: GFU-A0203Y1P
; CURRENT APPLICATION NUMBER: US/10/512,386
; CURRENT FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: JP 2002-127089
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: JP 2003-4706
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/449,860
; PRIOR FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 1924
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-512-386-56

Query Match      34.1%; Score 31; DB 6; Length 1924;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 GRLSYSR 11

Db      613 KGG--SASRRRLSSAS 626

RESULT 26
US-10-501-834-7
; Sequence 7, Application US/10501834
; Publication No. US20060088828A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Peter C., Ward, Christopher J., Rossetti, Sandro, and Torres,
; APPLICANT: Vicente E.
; TITLE OF INVENTION: Polycystic Kidney Disease Nucleic Acids
; TITLE OF INVENTION: and Proteins
; FILE REFERENCE: 07039/386US1
; CURRENT APPLICATION NUMBER: US/10/501,834
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: PCT/US03/02038
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 60/351,110
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 4051
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-501-834-7

Query Match      34.1%; Score 31; DB 6; Length 4051;
Best Local Similarity 70.0%; Pred. No. 1.3e+03;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      6 SYSRRRPFSTS 15
      |||||
Db      2256 SYMDRSFSTS 2265

RESULT 27
US-10-501-814-3
; Sequence 3, Application US/10501814
; Publication No. US20060088827A1
; GENERAL INFORMATION:
; APPLICANT: Evotec NeuroSciences GmbH
; TITLE OF INVENTION: Diagnostic and therapeutic use of a voltage-gated ion
; TITLE OF INVENTION: channel for neurodegenerative diseases
; FILE REFERENCE: P67564US1
; CURRENT APPLICATION NUMBER: US/10/501,814
; CURRENT FILING DATE: 2004-07-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2005
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-814-3

Query Match      33.5%; Score 30.5; DB 6; Length 2005;
Best Local Similarity 53.8%; Pred. No. 7e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY      2 GGRLSYSRPFST 14
      |||||
Db      543 GSRLTY-EKRFS 554

RESULT 28
US-11-263-326-131
; Sequence 131, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulvey, John C
; APPLICANT: Berkovic, Samuel F
```

```
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US 10/451,126
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 131
; LENGTH: 2005
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-131

Query Match      33.5%; Score 30.5; DB 7; Length 2005;
Best Local Similarity 53.8%; Pred. No. 7e+02; 2; Indels 1; Gaps 1;
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy      2  GGRLSYRRRRFST 14
Db      543  GSRLTY-EKRFSS 554

RESULT 29
US-11-263-326-132
; Sequence 132, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulvey, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 132
; LENGTH: 2005
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-132

Query Match      33.5%; Score 30.5; DB 7; Length 2005;
Best Local Similarity 53.8%; Pred. No. 7e+02; 2; Indels 1; Gaps 1;
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy      2  GGRLSYRRRRFST 14
Db      543  GSRLTY-EKRFSS 554

RESULT 30
US-11-263-326-133
; Sequence 133, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulvey, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 133
; LENGTH: 2005
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-133

Query Match      33.5%; Score 30.5; DB 7; Length 2005;
Best Local Similarity 53.8%; Pred. No. 7e+02; 2; Indels 1; Gaps 1;
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy      2  GGRLSYRRRRFST 14
Db      543  GSRLTY-EKRFSS 554

RESULT 31
US-11-263-326-175
; Sequence 175, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulvey, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 175
; LENGTH: 2005
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-175

Query Match      33.5%; Score 30.5; DB 7; Length 2005;
Best Local Similarity 53.8%; Pred. No. 7e+02; 2; Indels 1; Gaps 1;
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy      2  GGRLSYRRRRFST 14
Db      543  GSRLTY-EKRFSS 554

RESULT 32
US-11-263-326-176
; Sequence 176, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulvey, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
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; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 176
; LENGTH: 2005
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-176

Query Match 33.5%; Score 30.5; DB 7; Length 2005;
Best Local Similarity 53.8%; Pred. No. 7e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 GGRLSYRRRFFST 14
Db 543 GSRLTY-EKRFSS 554

RESULT 33
US-11-263-326-177
; Sequence 177, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 177
; LENGTH: 2005
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-177

Query Match 33.5%; Score 30.5; DB 7; Length 2005;
Best Local Similarity 53.8%; Pred. No. 7e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 GGRLSYRRRFFST 14
Db 543 GSRLTY-EKRFSS 554

RESULT 34
US-11-263-326-178
; Sequence 178, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126

; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 178
; LENGTH: 2005
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-178

Query Match 33.5%; Score 30.5; DB 7; Length 2005;
Best Local Similarity 53.8%; Pred. No. 7e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 GGRLSYRRRFFST 14
Db 543 GSRLTY-EKRFSS 554

RESULT 35
US-11-263-326-179
; Sequence 179, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 179
; LENGTH: 2005
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-263-326-179

Query Match 33.5%; Score 30.5; DB 7; Length 2005;
Best Local Similarity 53.8%; Pred. No. 7e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 GGRLSYRRRFFST 14
Db 543 GSRLTY-EKRFSS 554

RESULT 36
US-11-301-924-24
; Sequence 24, Application US/11301924
; Publication No. US20060090218A1
; GENERAL INFORMATION:
; APPLICANT: Joshua Z. Levin
; APPLICANT: Ken Phillips
; APPLICANT: Greg Budziszewski
; APPLICANT: Fred Meins
; APPLICANT: Zhenya Glazov
; TITLE OF INVENTION: Methods of Controlling Gene Expression
; FILE REFERENCE: 31481USNP
; CURRENT APPLICATION NUMBER: US/11/301,924
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US/09/896,186
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/222,202
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 24
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-301-924-24

Query Match      33.0%; Score 30; DB 7; Length 288;
Best Local Similarity 62.5%; Pred. No. 94;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GGRLSYSR 9
Db      95 GGRILYSK 102

RESULT 37
US-11-246-957-16
; Sequence 16, Application US/11246957
; Publication No. US20060093621A1
; GENERAL INFORMATION:
; APPLICANT: Bandara, Aloka
; APPLICANT: Boyle, Stephen
; APPLICANT: Sriranganathan, Nammalwar
; APPLICANT: Schurig, Gerhard
; TITLE OF INVENTION: Development of a Live, Attenuated, Recombinant Vaccine for
; TITLE OF INVENTION: Brucellosis
; FILE REFERENCE: 01640446pa
; CURRENT APPLICATION NUMBER: US/11/246,957
; PRIOR FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US60/541,954
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US 11/050,429
; PRIOR FILING DATE: 2005-02-04
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Bradyrhizobium japonicum
US-11-246-957-16

Query Match      33.0%; Score 30; DB 7; Length 298;
Best Local Similarity 37.5%; Pred. No. 98;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy      3 GRLSYRRRPFSTGTGR 18
Db      282 GALALTARYTTPSGR 297

RESULT 38
US-11-301-924-2
; Sequence 2, Application US/11301924
; Publication No. US20060090218A1
; GENERAL INFORMATION:
; APPLICANT: Joshua Z. Levin
; APPLICANT: Ken Phillips
; APPLICANT: Greg Budziszewski
; APPLICANT: Fred Meins
; APPLICANT: Zhenya Glazov
; TITLE OF INVENTION: Methods of Controlling Gene Expression
; FILE REFERENCE: 31481USNP
; CURRENT APPLICATION NUMBER: US/11/301,924
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US/09/896,186
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/222,202
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 313
; TYPE: PRT
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; ORGANISM: Arabidopsis thaliana
US-11-301-924-2

Query Match      33.0%; Score 30; DB 7; Length 313;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GGRLSYSR 9
Db      95 GGRILYSK 102

RESULT 39
US-10-511-937-2466
; Sequence 2466, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2466
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2466

Query Match      33.0%; Score 30; DB 6; Length 362;
Best Local Similarity 42.9%; Pred. No. 1.2e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy      3 GRLSYRRRPFSTST 16
Db      267 GRRSWARKQAHT 280

RESULT 40
US-10-511-937-2608
; Sequence 2608, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
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; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2608
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2608

Query Match 33.0%; Score 30; DB 6; Length 362;
Best Local Similarity 53.8%; Pred.No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 6 SYSRRRFSTGTGR 18
|:|:|:|:|
Db 26 SHSMRYFTTSVSR 38

Search completed: May 21, 2006, 00:39:35
Job time : 10 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 21, 2006, 00:19:21 ; Search time 38 Seconds
(without alignments)
45.576 Million cell updates/sec

Title: US-09-857-000a-11
Perfect score: 91
Sequence: 1 RGRLSYRRRSTSTGR 18

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: PIR 80.*
2: PIR1.*
3: PIR2.*
4: PIR3.*
5: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	67.0	149	2 S57607	protegrin 1 precu
2	55	60.4	147	2 JN0900	protegrin 2 precu
3	54	59.3	149	2 A53895	protegrin 3 precu
4	54	59.3	149	2 S57609	protegrin 5 precu
5	47	51.6	94	1 B48549	nucleic acid-bindi
6	47	51.6	447	2 S53982	hypothetical prote
7	46	50.5	231	2 T32047	hypothetical prote
8	45	49.5	191	1 QOAG6T	hypothetical prote
9	44	48.4	186	2 A30832	hypothetical prote
10	44	48.4	186	2 AC3229	protein 6a [import
11	44	48.4	293	2 D81896	Neisseria meningit
12	44	48.4	413	2 T03240	FlO/LFY protein ho
13	44	48.4	475	2 B89978	glutamyl-trnAGln a
14	44	48.4	532	2 H2730	probable acyl-CoA
15	43	47.3	107	2 J01251	hypothetical 12.6K
16	43	47.3	108	1 WNVTF5	nucleic acid-bindi
17	43	47.3	108	2 S12976	12K protein - pota
18	43	47.3	337	2 A10079	probable glycoprot
19	42	46.2	118	2 C72642	hypothetical prote
20	42	46.2	210	2 AB3420	hypothetical phage
21	42	46.2	386	2 A41950	retrovirus-related
22	42	46.2	747	2 T42599	minor capsid prote
23	42	46.2	1016	2 T30943	aminopeptidase (EC
24	42	46.2	1016	2 T30942	aminopeptidase (EC
25	41	45.1	201	2 B72739	hypothetical prote
26	41	45.1	310	2 T43147	hypothetical prote
27	41	45.1	325	2 T38308	hypothetical prote
28	41	45.1	390	2 AC2761	penicillin binding
29	41	45.1	413	2 A97542	D-ala-D-ala-carbox

30	41	45.1	547	2 S53920	SNG1 protein - yea
31	41	45.1	618	2 AC0884	glutathionylpermi
32	41	45.1	619	2 A91113	glutathionylpermi
33	41	45.1	619	2 A85958	glutathionylpermi
34	41	45.1	619	2 A57538	glutathionylpermi
35	40.5	44.5	464	2 A56800	intermediate filam
36	40	44.0	76	2 A87655	ribosomal protein
37	40	44.0	217	2 T33652	hypothetical prote
38	40	44.0	352	2 D96597	hypothetical prote
39	40	44.0	499	2 C85022	hypothetical prote
40	40	44.0	508	1 O4CHC7	steroid 17alpha-mo
41	40	44.0	513	2 T02002	hypothetical prote
42	40	44.0	622	2 A70414	hypothetical prote
43	40	44.0	622	2 I37984	NADH2 dehydrogenas
44	40	44.0	743	2 E71432	keratin 9, type I,
45	40	44.0	901	2 A13592	hypothetical prote
46	40	44.0	1030	2 A13592	DNA topoisomerase
47	40	44.0	1224	2 T16114	hypothetical prote
48	40	44.0	1636	2 T26377	hypothetical prote
49	39.5	43.4	333	2 AC2386	hypothetical prote
50	39	42.9	51	2 G70154	chaperone DnaJ pro
51	39	42.9	105	2 S42214	ribosomal protein
52	39	42.9	105	2 S42213	hydroxymethylgluta
53	39	42.9	119	2 D82387	conserved hypotet
54	39	42.9	159	2 T05656	hypothetical prote
55	39	42.9	188	2 A48024	glycosylphosphatid
56	39	42.9	211	2 C84888	hypothetical prote
57	39	42.9	231	2 A71838	hypothetical prote
58	39	42.9	245	2 D84179	hypothetical prote
59	39	42.9	262	2 A13518	nitrate reductase
60	39	42.9	351	2 B34768	ORF5 protein - Orf
61	39	42.9	361	2 B82533	translation releas
62	39	42.9	377	2 E83220	hypothetical prote
63	39	42.9	475	2 AD2698	molecular chaperon
64	39	42.9	533	2 D97480	probable heat-shoc
65	39	42.9	661	2 H84406	aconitase [import
66	39	42.9	694	2 F82511	vgrG protein VCA00
67	39	42.9	753	1 WZBE8	gene 56 protein -
68	39	42.9	865	2 B69074	probable formate d
69	39	42.9	873	2 B87049	conserved hypotet
70	39	42.9	883	2 C83385	hypothetical prote
71	39	42.9	1163	2 D82202	vgrG protein VCI41
72	39	42.9	2248	2 A35938	profilaggrin - hum
73	38	41.8	135	2 C95422	TRM2011-2a transpo
74	38	41.8	135	2 B95386	TRM2011-2a transpo
75	38	41.8	135	2 A95263	TRM2011-2a transpo
76	38	41.8	135	2 H95878	probable ISM2011-
77	38	41.8	135	2 C96026	probable transposa
78	38	41.8	136	2 E95401	TRM2011-2a transpo
79	38	41.8	149	2 B53895	protegrin 4 precu
80	38	41.8	182	2 A02947	keratin, 60K type
81	38	41.8	213	2 T01464	hypothetical prote
82	38	41.8	218	2 E85021	hypothetical prote
83	38	41.8	276	2 D70817	hypothetical prote
84	38	41.8	313	2 A84444	filaggrin precurs
85	38	41.8	341	2 H83572	O-sialoglycoprotei
86	38	41.8	438	2 A57219	Batten disease-rel
87	38	41.8	438	2 C69431	signal-transducin
88	38	41.8	476	2 AB1294	glutamyl-tRNA(Gln)
89	38	41.8	476	2 AB1665	glutamyl-tRNA(Gln)
90	38	41.8	488	2 E86645	Glu-tRNA amidotran
91	38	41.8	491	2 T21421	hypothetical prote
92	38	41.8	529	1 H70736	IMP dehydrogenase
93	38	41.8	558	2 T50595	probable alkaline
94	38	41.8	590	2 A29904	keratin 5, type II
95	38	41.8	902	2 D84970	ribonuclease 8 [im
96	37.5	41.2	196	2 E84638	probable RS2p22 sp
97	37.5	41.2	358	2 I38121	protein kinase - h
98	37	40.7	219	1 TRPGAZ	azurocidin - pig
99	37	40.7	219	2 C69439	sugar fermentation
100	37	40.7	315	2 D84139	mannose-6-phosphat

ALIGNMENTS

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RESULT 1
S57607
protegrin 1 precursor - pig
N/Alternate names: neutrophil peptide 1
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C/Accession: S66284; S45712; S36820; S34585; S57607
R/Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A/Title: The structure of porcine protegrin genes.
A/Reference number: S66284; MUID:95354835; PMID:7628604
A/Accession: S66284
A/Molecule type: DNA
A/Residues: 1-149 <ZHA>
A/Cross-references: UNIPROT:P32194; UNIPARC:UPI0000131775; EMBL:X84094; NID:g887642; PID:
R/Zhao, C.; Liu, L.; Lehrer, R.I.
FEBS Lett. 346, 285-288, 1994
A/Title: Identification of a new member of the protegrin family by cDNA cloning.
A/Reference number: S45712; MUID:94283613; PMID:8013647
A/Accession: S45712
A/Molecule type: mRNA
A/Residues: 1-149 <ZH2>
A/Cross-references: UNIPARC:UPI0000131775; GB:X79868; NID:g603035; PIDN:CAA56251.1; PID:
R/Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov,
FEBS Lett. 330, 339-342, 1993
A/Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence
A/Reference number: S36820; MUID:93387466; PMID:8375505
A/Accession: S36820
A/Molecule type: protein
A/Residues: 131-148 <MIR>
A/Cross-references: UNIPROT:P32194; UNIPARC:UPI000014310F
R/Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Alezhina, G.M.; She
FEBS Lett. 327, 231-236, 1993
A/Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost
A/Reference number: S34585; MUID:93327946; PMID:8335113
A/Accession: S34586
A/Molecule type: protein
A/Residues: 131-146 <KOK>
A/Cross-references: UNIPARC:UPI000014310F
C/Comment: This protein plays a role in the nonoxidative antimicrobial defense mechanisms
C/Superfamily: cathelin; cystatin homology
C/Keywords: amidated carboxyl end; antibacterial; neutrophil
F/1-29/Domain: signal sequence #status predicted <SIG>
F/22-129/Domain: cystatin homology <CYS>
F/131-146/Product: protegrin 2 #status experimental <MAT>
F/148/Modified site: amidated carboxyl end (Val) (amide in mature form from following gl
A/Query Match 67.0%; Score 61; DB 2; Length 149;
Best Local Similarity 66.7%; Pred. No. 0.0087;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18
DB 131 RGGRLCYRRRFFCVGVR 148

RESULT 2
JN0900
protegrin 2 precursor - pig
N/Alternate names: cathelin-like protein precursor; neutrophil peptide 3
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C/Accession: JN0900; S36822; S34586
R/Storici, P.; Zanetti, M.
Biochem. Biophys. Res. Commun. 196, 1363-1368, 1993
A/Title: A novel cDNA sequence encoding a pig leukocyte antimicrobial peptide with a cat
A/Reference number: S36820; MUID:94071898; PMID:8250892
```

```
A/Accession: JN0900
A/Molecule type: mRNA
A/Residues: 1-147 <STO>
A/Cross-references: UNIPROT:P32195; UNIPARC:UPI0000131776; GB:I24745; NID:g431435; PIDN:
R/Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov,
FEBS Lett. 330, 339-342, 1993
A/Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence
A/Reference number: S36820; MUID:93387466; PMID:8375505
A/Accession: S36822
A/Molecule type: protein
A/Residues: 131-146 <MIR>
A/Cross-references: UNIPARC:UPI000014310F
R/Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Alezhina, G.M.; She
FEBS Lett. 327, 231-236, 1993
A/Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost
A/Reference number: S34585; MUID:93327946; PMID:8335113
A/Accession: S34586
A/Molecule type: protein
A/Residues: 131-146 <KOK>
A/Cross-references: UNIPARC:UPI000014310F
C/Comment: This protein plays a role in the nonoxidative antimicrobial defense mechanisms
C/Superfamily: cathelin; cystatin homology
C/Keywords: amidated carboxyl end; antibacterial; neutrophil
F/1-29/Domain: signal sequence #status predicted <SIG>
F/22-129/Domain: cystatin homology <CYS>
F/131-146/Product: protegrin 2 #status experimental <MAT>
F/148/Modified site: amidated carboxyl end (Val) (amide in mature form from following gl
A/Query Match 60.4%; Score 55; DB 2; Length 147;
Best Local Similarity 64.7%; Pred. No. 0.086;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTG 17
DB 131 RGGRLCYRRRFFCICVG 147

RESULT 3
A53895
protegrin 3 precursor - pig
N/Alternate names: neutrophil peptide 2
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C/Accession: S66285; A53895; S34587; S36821; S57608
R/Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A/Title: The structure of porcine protegrin genes.
A/Reference number: S66283; MUID:95354835; PMID:7628604
A/Accession: S66285
A/Molecule type: DNA
A/Residues: 1-149 <ZH3>
A/Cross-references: UNIPROT:P32196; UNIPARC:UPI0000131777; EMBL:X84095; NID:g887644; PID:
R/Zhao, C.; Liu, L.; Lehrer, R.I.
FEBS Lett. 346, 285-288, 1994
A/Title: Identification of a new member of the protegrin family by cDNA cloning.
A/Reference number: S45712; MUID:94283613; PMID:8013647
A/Accession: A53895
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-149 <ZHA>
A/Cross-references: UNIPARC:UPI0000131777; GB:X83267; NID:g603037; PIDN:CAA58240.1; PID:
R/Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Alezhina, G.M.; She
FEBS Lett. 327, 231-236, 1993
A/Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost
A/Reference number: S34585; MUID:93327946; PMID:8335113
A/Accession: S34587
A/Molecule type: protein
A/Residues: 131-148 <KOK>
A/Cross-references: UNIPARC:UPI0000143110
R/Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov,
FEBS Lett. 330, 339-342, 1993
A/Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence
A/Reference number: S36820; MUID:93387466; PMID:8375505
```


A;Cross-references: UNIPROT:Q86541; UNIPARC:UPI00000P9P61; GB:S45593; NID:G256417; PIDN: C;Note: sequence extracted from NCBI backbone (NCBIN:114637, NCBIP:114639)
C;Superfamily: potato virus nucleic acid-binding protein
C;Keywords: DNA binding; zinc finger
F;55-75/Region: zinc finger

Query Match 51.6%; Score 47; DB 1; Length 94;
Best Local Similarity 52.9%; Pred. No. 1.2;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYSRRRPFSTGTGR 18
||| :|:| :||
DB 38 GGRSTYAKRRARSIGR 54
||| :|:| :||

RESULT 6
S53982
hypothetical protein 447 - actinophaga RP3
C;Species: actinophaga RP3
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S53982
R;Gabriel, K.; Schmid, H.; Schmidt, U.; Rausch, H.
Nucleic Acids Res. 23, 59-63, 1995
A;Title: The actinophaga RP3 DNA integrates site-specifically into the putative tRNA(Arg
A;Reference number: S53981; MUID:95175370; PMID:7870591
A;Accession: S53982
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-447 <GAB>
A;Cross-references: UNIPARC:UPI000017A848; EMBL:X80661
C;Genetics:
A;Start codon: GTG

Query Match 51.6%; Score 47; DB 2; Length 447;
Best Local Similarity 47.1%; Pred. No. 5.3;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 RGGRLYSRRRPFSTGTG 17
||| :|:| :||
DB 9 RGGSVAVAEKRVSTAKG 25
||| :|:| :||

RESULT 7
T32047
hypothetical protein K07E8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32047
R;Jones, K.; Kramer, J.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid K07E8.
A;Reference number: Z21116
A;Accession: T32047
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-231 <JON>
A;Cross-references: UNIPROT:O16689; UNIPARC:UPI000017BA9P; EMBL:AF016678; PIDN:AAB66149.1
A;Experimental source: strain Bristol N2; clone K07E8
C;Genetics:
A;Gene: CESP:K07E8.3
A;Map position: 2
A;Introns: 69/3; 104/1; 171/3; 203/3

Query Match 50.5%; Score 46; DB 2; Length 231;
Best Local Similarity 47.1%; Pred. No. 4.1;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLYSRRRPFSTGTG 17
||| :|:| :||
DB 74 RGGRVYHDKRYPNRTG 90
||| :|:| :||

RESULT 8

QOAG6T
hypothetical protein 6 - Agrobacterium tumefaciens plasmids
C:Species: Agrobacterium tumefaciens
C>Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
R:Gielen, J.; De Beuckeleer, M.; Seurinck, J.; Deboeck, P.; De Greve, H.; Lemmers, M.; VEMBO J. 3, 835-846, 1984
A:Title: The complete nucleotide sequence of the TL-DNA of the Agrobacterium tumefaciens
A:Reference number: A91001; MUID:84207942; PMID:6327292
A:Accession: A04498
A:Molecule type: DNA
A:Residues: 1-191 <GIE>
A:Cross-references: UNIPROT:P04030; UNIPARC:UPI00000008AB; GB:X00493; GB:J05108; GB:X002
A:Experimental source: plasmid pRIach5
R:Barker, R.F.; Idler, K.B.; Thompson, D.V.; Kemp, J.D.
Plant Mol. Biol. 2, 335-350, 1983
A:Title: Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens octo
A:Reference number: S28683
A:Accession: S28691
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-191 <BAR>
A:Cross-references: UNIPARC:UPI00000008AB; EMBL:X00493; NID:g39062; PIDN:CAA25171.1; PID
A:Experimental source: plasmid pT115955
C:Genetics:
A:Genome: plasmid
C:Superfamily: T-6b protein
C:Keywords: crown gall tumor

Query Match 49.5%; Score 45; DB 1; Length 191;
Best Local Similarity 50.0%; Pred. No. 5.1;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGRLSYSRRRFFSTS 15
Db 112 GGRINYSKNEYSSS 125
|||:|:|:|:|:|

RESULT 9
A30832
hypothetical protein 6a - Agrobacterium tumefaciens plasmid pTIT37
C:Species: Agrobacterium tumefaciens
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: A30832
R:Vanderleyden, J.; Desair, J.; De Meirsmann, C.; Michiels, K.; Van Gool, A.; Jen, G.; Ch
Plant Mol. Biol. 7, 33-41, 1986
A:Title: Nucleotide sequence of the T-DNA region encoding transcripts 6a and 6b of the E
A:Reference number: A93763
A:Accession: A30832
A:Molecule type: DNA
A:Residues: 1-186 <VAN>
A:Cross-references: UNIPROT:Q52604; UNIPARC:UPI000000B68A2
C:Genetics:
A:Genome: plasmid
C:Superfamily: T-6b protein

Query Match 48.4%; Score 44; DB 2; Length 186;
Best Local Similarity 57.1%; Pred. No. 7.2;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGRLSYSRRRFFSTS 15
Db 107 GGRINYSRNEHSSS 120
|||:|:|:|:|:|

RESULT 10
AC3229
protein 6a [imported] - Agrobacterium tumefaciens (strain C58, Dupont) plasmid Ti
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AC3229
R:Wood, D.W.; Secubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, H
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AC3229
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-186 <KUR>
A:Cross-references: UNIPROT:Q9R430; UNIPARC:UPI00000D609F; GB:AE008690; PIDN:AAL46249.1;
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: genes6
A:Genome: plasmid
C:Superfamily: T-6b protein

Query Match 48.4%; Score 44; DB 2; Length 186;
Best Local Similarity 57.1%; Pred. No. 7.2;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGRLSYSRRRFFSTS 15
Db 107 GGRINYSRNEHSSS 120
|||:|:|:|:|:|

RESULT 11
DB1896
Neisseria meningitidis hypothetical protein NMA1282 - Neisseria meningitidis (strain Z249
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: DB1896
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: AB1775; MUID:20222556; PMID:10761919
A:Accession: DB1896
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-293 <PAR>
A:Cross-references: UNIPROT:Q9JUJ7; UNIPARC:UPI00000C4B6C; GB:AL162755; GB:AL157959; NID:
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1282
C:Superfamily: Neisseria meningitidis hypothetical protein NMA1282

Query Match 48.4%; Score 44; DB 2; Length 293;
Best Local Similarity 57.1%; Pred. No. 11;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 RLSYSRRRFFSTGTG 17
Db 38 RLGSYRKNPAEQTG 51
|||:|:|:|:|:|

RESULT 12
T03240
FLO/LFY protein homolog NFL1 - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03240
R:Kelly, A.J.; Bonlander, M.B.; Meeks-Wagner, D.R.
Plant Cell 7, 225-234, 1995
A:Title: NFL, the tobacco homologue of FLORICAULA and LEAFY, is transcriptionally expres
A:Reference number: Z14855; MUID:95276463; PMID:7756832
A:Accession: T03240
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-413 <KEL>
A:Cross-references: UNIPROT:Q40504; UNIPARC:UPI000012A83A; EMBL:U16172; NID:g561681; PIDN
A:Experimental source: cultivar Sameun
C:Genetics:

A;Introns: 154/1; 288/3
C;Superfamily: Arabidopsis thaliana LFY floral meristem identity control protein
C;Keywords: transcription regulation

Query Match 48.4%; Score 44; DB 2; Length 413;
Best Local Similarity 52.9%; Pred. No. 15;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 GGRLSYSRRRPFSTGTGR 18
|||: ||: |||||
Db 186 GGRMKQRKKKVVSTGR 202

RESULT 13
B89978
glutamyl-tRNA ligase subunit B [imported] - Staphylococcus aureus (strain N
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B89978
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogino,
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: B89978
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-475 <KUR>
A;Cross-references: UNIPROT:Q9SVY7; UNIPARC:UPI000012B162; GB:BA000018; PID:g13701692; F
C;Experimental source: strain N315
C;Genetics:
A;Gene: SA1715
C;Superfamily: PET112 protein

Query Match 48.4%; Score 44; DB 2; Length 475;
Best Local Similarity 47.1%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 GGRLSYSRRRPFSTGTGR 18
|||: |||: |||:
Db 238 GGEIGQETRRPFDESTGK 254

RESULT 14
H72730
probable acyl-CoA dehydrogenase, short-chain specific APE0385 - Aeropyrum pernix (strain
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: H72730
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-532 <KAW>
A;Cross-references: UNIPROT:Q9YF56; UNIPARC:UPI000005DB09; DDBJ:AP0000059; NID:g5103911;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0385

Query Match 48.4%; Score 44; DB 2; Length 532;
Best Local Similarity 52.9%; Pred. No. 20;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRPFSTGTG 17
|||: |||: |||:
Db 222 RGGGLNYSVRLKDKSG 238

RESULT 15

JQ1251
hypothetical 12.6K protein - chrysanthemum virus B

C;Species: chrysanthemum virus B

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: JQ1251

R;Levay, K.; Zavrjev, S.

J. Gen. Virol. 72, 2333-2337, 1991

A;Title: Nucleotide sequence and gene organization of the 3'-terminal region of chrysanth

A;Reference number: JQ1246; MUID:92013948; PMID:1919520

A;Accession: JQ1251

A;Molecule type: genomic RNA

A;Residues: 1-107 <LEV>

A;Cross-references: UNIPROT:P37992; UNIPARC:UPI0000138A0A; GB:S60150; NID:g237315; PIDN:

C;Superfamily: potato virus nucleic acid-binding protein

Query Match 47.1%; Score 43; DB 2; Length 107;

Best Local Similarity 56.2%; Pred. No. 6.3;

Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 GRLSYSRRRPFSTGTGR 18

|||: |||: |||:

Db 40 GRSSVARRRRLGLR 55

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Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFFSTGTGR 18
||| :||| :|||
Db 40 GGRSKYARRRAISAR 56

RESULT 17
S12976
12K protein - potato virus M
C:Species: potato virus M
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S12976
R:Gramstat, A.; Courtopozanis, A.; Rohde, W.
FEBS Lett. 276, 34-38, 1990
A:Title: The 12 kDa protein of potato virus M displays properties of a nucleic acid-binding protein
A:Reference number: S12975; MUID:91092429; PMID:2265707
A:Accession: S12976
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-108 <GRA>
C:Cross-references: UNIPROT:Q01687; UNIPARC:UPI0000138A0E; GB:X57440; NID:G61400; PIDN:C
C:Superfamily: potato virus nucleic acid-binding protein

Query Match 47.3%; Score 43; DB 2; Length 108;
Best Local Similarity 52.9%; Pred. No. 6.3;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFFSTGTGR 18
||| :||| :|||
Db 40 GGRSKYARRRAISAR 56

RESULT 18
AI0079
probable glycoproteinase gcp [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AI0079
R:Parkhill, J.; Wren, B.W.; Thomsen, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AI0079
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-337 <KUR>
C:Cross-references: UNIPARC:UPI00000CD702; GB:AL590842; PIDN:CAC89500.1; PID:G15978736;
C:Genetics:
A:Gene: gcp
C:Superfamily: O-sialoglycoprotein endopeptidase

Query Match 47.3%; Score 43; DB 2; Length 337;
Best Local Similarity 47.1%; Pred. No. 19;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTG 17
||| :||| :|||
Db 286 RGGEVYFARPEFTDNG 302

RESULT 19
C72642
hypothetical protein APE0571 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: C72642
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr

A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: C72642
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-118 <KAW>
A:Cross-references: UNIPROT:Q9YBK7; UNIPARC:UPI000005DBD0; DDBJ:AF000060; NID:G5104188; I
C:Genetics:
A:Gene: APE0571

Query Match 46.2%; Score 42; DB 2; Length 118;
Best Local Similarity 81.8%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGGRLSYRRR 11
||| :||| :|||
Db 21 RGGRLSYRRR 31

RESULT 20
AB3420
hypothetical phage protein BME11344 [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AB3420
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, I
; Macur, M.; Goltzman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AB3252; PMID:11756688
A:Accession: AB3420
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-210 <KUR>
A:Cross-references: UNIPROT:Q8YGL8; UNIPROT:Q8G1V4; UNIPARC:UPI0000058029; GB:AE008917; I
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME11344
A:Map position: 1

Query Match 46.2%; Score 42; DB 2; Length 210;
Best Local Similarity 47.1%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTG 17
||| :||| :|||
Db 38 RNARWAHSRRHFDAGTG 54

RESULT 21
A41950
retrovirus-related hypothetical protein 1 - Trypanosoma cruzi retrotransposon
C:Species: Trypanosoma cruzi
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Jan-1999
C:Accession: A41950
R:Villanueva, M.S.; Williams, S.P.; Beard, C.B.; Richards, F.F.; Aksoy, S.
Mol. Cell. Biol. 11, 6139-6148, 1991
A:Title: A new member of a family of site-specific retrotransposons is present in the spi
A:Reference number: A41950; MUID:92049344; PMID:1719380
A:Accession: A41950
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-386 <VIL>
A:Cross-references: UNIPARC:UPI000011DB57; GB:M62862; NID:G162247; PID:G162248
A:Note: sequence extracted from NCBI backbone (NCBIN:66378, NCSIP:66379)

Query Match 46.2%; Score 42; DB 2; Length 386;
Best Local Similarity 44.4%; Pred. No. 31;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRFFSTGTGR 18
||| :||| :|||
Db 153 KGGRAGVATRRFSGTTNQ 170

A;Cross-references: UNIPROT:O17484; UNIPARC:UPI000007F70A; EMBL:AF034483; NID:g2645992;
C;Superfamily: membrane alanyl aminopeptidase
C;Keywords: aminopeptidase

Query Match 46.2%; Score 42; DB 2; Length 1016;
Best Local Similarity 53.3%; Pred. No. 77;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 GRLSYRRRPFSTGT 17
|||:||||:
Db 555 GRLTISQRFDITNG 569

RESULT 25
B72739
hypothetical protein APE0444 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: B72739
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Takah
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: B72739
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-201 <RAW>
A;Cross-references: UNIPROT:Q9VEZ0; UNIPARC:UPI000005DB4B; DDBJ:AP0000059; NID:gs103911;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0444

Query Match 45.1%; Score 41; DB 2; Length 201;
Best Local Similarity 56.2%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 GGRLSYRRRPFSTGT 17
|||:||||:
Db 70 GGLFSYSLRRVSREAG 85

RESULT 26
T43147
hypothetical protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43147
R;Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A;Title: Identification of open reading frames in Schizosaccharomyces pombe CDNAS.
A;Reference number: Z17323; MUID:98162722; PMID:9501991
A;Accession: T43147
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-310 <YOS>
A;Cross-references: UNIPROT:P78890; UNIPARC:UPI000016911B; EMBL:D89241; NID:gl749689; PFI
A;Experimental source: strain PR745

Query Match 45.1%; Score 41; DB 2; Length 310;
Best Local Similarity 60.0%; Pred. No. 37;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RGRLSYRRRPFSTGT 15
|||:||||:
Db 96 RGGDTSYSLRRHDDSS 110

RESULT 27
T38308
hypothetical protein SPAC23H3.15c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

minor capsid protein 56 - equine herpesvirus 4 (strain NS80567)
A;Variety: strain NS80567
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42599
R;Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
J. Gen. Virol. 79, 1197-1203, 1998
A;Title: The DNA sequence of equine herpesvirus-4.
A;Reference number: Z22173; MUID:98264497; PMID:9603335
A;Accession: T42599
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-747 <TEL>
A;Cross-references: UNIPROT:O39296; UNIPARC:UPI00000F3185; EMBL:AF030027; NID:g2605950;
A;Experimental source: strain NS80567
C;Genetics:
A;Note: 56
C;Superfamily: varicella-zoster virus gene 54 protein

Query Match 46.2%; Score 42; DB 2; Length 747;
Best Local Similarity 55.6%; Pred. No. 58;
Matches 10; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 RGRLSYRRRPFSTGT 18
|||:||||:
Db 700 RGGGYKRRFPNSYSR 717

RESULT 23
T30943
aminopeptidase (SC 3.4.11.-) - Indian meal moth
C;Species: Plodia interpunctella (Indian meal moth)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: T30943
R;Zhu, Y.C.; Oppert, B.; Kramer, K.J.; McGaughey, W.H.; Dowdy, A.K.
submitted to the EMBL Data Library, November 1997
A;Description: Molecular comparison of aminopeptidase cDNAs and gene structure between
A;Reference number: Z20942
A;Accession: T30943
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1016 <ZHU>
A;Cross-references: UNIPROT:O17485; UNIPARC:UPI0000078275; EMBL:AF034484; NID:g2645994;
C;Superfamily: membrane alanyl aminopeptidase
C;Keywords: aminopeptidase

Query Match 46.2%; Score 42; DB 2; Length 1016;
Best Local Similarity 53.3%; Pred. No. 77;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 GRLSYRRRPFSTGT 17
|||:||||:
Db 555 GRLTISQRFDITNG 569

RESULT 24
T30942
aminopeptidase (SC 3.4.11.-) - Indian meal moth
C;Species: Plodia interpunctella (Indian meal moth)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: T30942
R;Zhu, Y.C.; Oppert, B.; Kramer, K.J.; McGaughey, W.H.; Dowdy, A.K.
submitted to the EMBL Data Library, November 1997
A;Description: Molecular comparison of aminopeptidase cDNAs and gene structure between
A;Reference number: Z20942
A;Accession: T30942
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1016 <ZHU>

C;Accession: T38308; T38381
R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21785
A;Accession: T38308
A;Molecule type: DNA
A;Residues: 1-325 <SKE>
A;Cross-references: UNIPROT:P78890; UNIPARC:UPI000006C8C6; EMBL:Z99163; PIDN:CAB16245.1;
A;Experimental source: strain 972h-; cosmid c23H3
R;Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z21737
A;Accession: T38381
A;Molecule type: DNA
A;Residues: 1-87 <DEV>
A;Cross-references: UNIPARC:UPI0000169022; EMBL:Z98944; PIDN:CAB11598.1; GSPDB:GN000066;
A;Experimental source: strain 972h-; cosmid c25H1
C;Genetics:
A;Gene: SPAC23H3.15c; SPDB:SPAC25H1.01c
A;Map position: 1

Query Match 45.1%; Score 41; DB 2; Length 325;
Best Local Similarity 60.0%; Pred. No. 39;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RGRLSYSRRRPFSTS 15
||| ||||| :||
Db 96 RGGDTYSRRHDDSS 110

RESULT 28
AC2761
penicillin binding protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AC2761
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AC2761
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-390 <KUR>
A;Cross-references: UNIPROT:Q8UF99; UNIPARC:UPI0000164602; GB:AE008688; PIDN:AAL42505.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: dac
A;Map position: circular chromosome

Query Match 45.1%; Score 41; DB 2; Length 390;
Best Local Similarity 52.9%; Pred. No. 46;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 RGRLSYSRRRPFSTG 17
||| ||||| :|||
Db 155 RAGELGMRNRSIFSSTG 171

RESULT 29
A97542
D-ala-D-ala-carboxypeptidase (PA3999) [imported] - Agrobacterium tumefaciens (strain C58)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: A97542
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: A97542
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-413 <KUR>
A;Cross-references: UNIPROT:Q8UF99; UNIPARC:UPI00000D1B95; GB:AE007869; PIDN:AAK87290.1;
C;Genetics:
A;Gene: AGR_C_2763
A;Map position: circular chromosome

Query Match 45.1%; Score 41; DB 2; Length 413;
Best Local Similarity 52.9%; Pred. No. 48;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 RGRLSYSRRRPFSTG 17
||| ||||| :|||
Db 178 RAGELGMRNRSIFSSTG 194

RESULT 30
S53920
SNG1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein G4883; protein G7591; protein YGR197c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S53920; S53895; S59182; S64515; S64519
R;Nombela, C.
submitted to the EMBL Data Library, November 1994
A;Reference number: S53918
A;Accession: S53920
A;Molecule type: DNA
A;Residues: 1-547 <NOM>
A;Cross-references: UNIPROT:P46950; UNIPARC:UPI000004F91B; EMBL:X82775; NID:g791126; PID:
R;Grey, M.
submitted to the EMBL Data Library, September 1993
A;Reference number: S53895
A;Accession: S53895
A;Molecule type: DNA
A;Residues: 1-116, 'V', 118-547 <GRE>
A;Cross-references: UNIPARC:UPI000016883D; EMBL:X74920; NID:g7633390; PID:g7633391
R;Guereiro, P.; Silva, A.M.E.; Barreiros, T.; Atroyo, J.; Garcia-Gonzalez, M.; Garcia-S-
Yeast 11, 1087-1091, 1995
A;Title: The complete sequence of a 9000 bp fragment of the right arm of Saccharomyces ce
A;Reference number: S59180; MUID:96076633; PMID:7502584
A;Accession: S59182
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-547 <GUE>
A;Cross-references: UNIPARC:UPI000004F91B; EMBL:X82775; NID:g791126; PIDN:CAA58016.1; PII
R;Arroyo, J.; Garcia-Gonzalez, M.; Garcia-Saez, M.I.; Sanchez-Perez, M.; Nombela, C.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64499
A;Accession: S64515
A;Molecule type: DNA
A;Residues: 1-547 <ARR>
A;Cross-references: UNIPARC:UPI000004F91B; EMBL:Z72982; NID:g1323350; PID:e243736; PID:g1
A;Experimental source: strain S288C
R;Guereiro, P.; Barreiros, T.; Cyrne, L.; Soares, H.; Maia e Silva, A.; Rodrigues-Pousa-
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64517
A;Accession: S64519
A;Molecule type: DNA
A;Residues: 1-547 <GUW>
A;Cross-references: UNIPARC:UPI000004F91B; EMBL:Z72982; NID:g1323350; PID:e243736; PID:g1
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:SNGL
A;Cross-references: SGD:S0003429; MIPS:YGR197C
A;Map position: 7R
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YOR015W
C;Keywords: transmembrane protein
F;110-126/Domain: transmembrane #status predicted <TM1>
F;318-334/Domain: transmembrane #status predicted <TM2>

F;367-383/Domain: transmembrane #status predicted <TM3>
 F;417-433/Domain: transmembrane #status predicted <TM4>
 F;488-504/Domain: transmembrane #status predicted <TM5>

Query Match 45.1%; Score 41; DB 2; Length 547;
 Best Local Similarity 50.0%; Pred. No. 63;
 Matches 9; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

Qy 2 GGR--LSYSRRRSTSTG 17
 |||:||||:|:|:
 Db 26 GGRDGVSYNQRFAGSG 43

RESULT 31

AC0884

glutathionylspermidine synthetase/amidase [imported] - Salmonella enterica subsp. enterica
 C;Species: Salmonella enterica subsp. enterica serovar Typhi
 A;Note: this species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AC0884
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AC0884

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-618 <PAR>

A;Cross-references: UNIPARC:UPI000005A46A; GB:AL513382; PIDN:CAD02971.1; PID:gl6504219;

C;Genetics:

A;Gene: STY3310

Query Match 45.1%; Score 41; DB 2; Length 618;
 Best Local Similarity 60.0%; Pred. No. 71;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 RLSYSRRRSTSTGR 18
 |||:||||
 Db 301 RLSWQRRRHMITGR 315

RESULT 32

A91113

glutathionylspermidine synthetase/amidase [imported] - Escherichia coli (strain O157:H7,
 C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: A91113

R;Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gagawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: A91113

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-619 <HAY>

A;Cross-references: UNIPROT:Q9XBW3; UNIPARC:UPI00000D054F; GB:BA000007; PIDN:BA837296.1;

A;Experimental source: strain O157:H7, substrain RIMD 0509952

C;Genetics:

A;Gene: ECs3873

Query Match 45.1%; Score 41; DB 2; Length 619;
 Best Local Similarity 60.0%; Pred. No. 71;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 RLSYSRRRSTSTGR 18
 |||:||||
 Db 302 RLSWQRRRHMITGR 316

RESULT 33

A85958

glutathionylspermidine synthetase/amidase [imported] - Escherichia coli (strain O157:H7,
 C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: A85958

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: A85958

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-619 <STO>

A;Cross-references: UNIPROT:Q9XBW3; UNIPARC:UPI00000D054F; GB:AE005174; NID:gl2517552; P

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: gap

Qy 4 RLSYSRRRSTSTGR 18
 |||:||||
 Db 302 RLSWQRRRHMITGR 316

RESULT 34

A57538

glutathionylspermidine synthetase/amidase - Escherichia coli (strain K-12)

C;Species: Escherichia coli

C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004

C;Accession: A57538; B65085

R;Boelling J.F. J.M.; Kwon, D.S.; Huisman, G.W.; Kolter, R.; Walsh, C.T.

J. Biol. Chem. 270, 14031-14041, 1995

A;Title: Glutathionylspermidine metabolism in Escherichia coli. Purification, cloning, o

A;Reference number: A57538; MUID:95294007; PMID:7775463

A;Accession: A57538

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-619 <BOL>

A;Cross-references: UNIPROT:P43675; UNIPARC:UPI000012BC7C; GB:U23148; NID:g861185; PIDN:AA

R;Blattner, P.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: B65085

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-619 <BLAT>

A;Cross-references: UNIPARC:UPI000012BC7C; GB:AE000381; GB:U00096; NID:g2367181; PIDN:AA

A;Experimental source: strain K-12, substrain MGL655

C;Genetics:

A;Gene: gap

C;Keywords: multifunctional enzyme

Qy 4 RLSYSRRRSTSTGR 18
 |||:||||
 Db 302 RLSWQRRRHMITGR 316

RESULT 35

A56600

intermediate filament protein IF-1, cytosolic - common lancelet

C;Species: Branchiostoma lanceolatum (common lancelet)

C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004

C;Accession: A56600; S24265
R;Riemer, D.; Dodemont, H.; Weber, K.
Eur. J. Cell Biol. 58, 128-135, 1992
A;Title: Analysis of the cDNA and gene encoding a cytoplasmic intermediate filament (IF) anily.
A;Reference number: A56600; MUID:92354564; PMID:1644059
A;Accession: A56600
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-464 <RIE>
A;Cross-references: UNIPROT:Q04948; UNIPARC:UPI000012D3D5; EMBL:X64522; NID:g5724; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIP:110465)
A;Note: intron positions were also determined
C;Superfamily: cytoskeletal keratin
C;Keywords: cytosol; intermediate filament

Query Match 44.5%; Score 40.5; DB 2; Length 464;
Best Local Similarity 61.1%; Pred. No. 66;
Matches 11; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 2 GGRLSYSRR-RFSTSTGR 18
||| ||| ||| ||| |||
DB 25 GGRASYSSGSRFGSGGGR 42

RESULT 36
ribosomal protein l31 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
A;Accession: A87655
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87655
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-76 <STO>
A;Cross-references: UNIPROT:Q9A3C9; UNIPARC:UPI0000133F04; GB:AE005673; NID:g13424965; H
C;Genetics:
A;Gene: CC3275

Query Match 44.0%; Score 40; DB 2; Length 76;
Best Local Similarity 44.4%; Pred. No. 14;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 RGGRLSYRRRPFSTSTGR 18
||| ||| ||| ||| |||
DB 57 RGGRVSRFNAKFAFTGK 74

RESULT 37
T33652
hypothetical protein T06A10.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
A;Accession: T33652
R;Zhu, H.; Hinds, K.; Keppler, D.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid T06A10.
A;Reference number: Z21382
A;Accession: T33652
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-217 <ZHU>
A;Cross-references: UNIPARC:UPI000017EB68; EMBL:AF099926; PIDN:AAC68906.1; GSFDB:GN00022
A;Experimental source: strain Bristol N2; clone T06A10
C;Genetics:
A;Gene: CESP:T06A10.2
A;Map position: 4

A;Introns: 30/3; 71/3; 105/3; 124/2; 172/1

Query Match 44.0%; Score 40; DB 2; Length 217;
Best Local Similarity 57.1%; Pred. No. 39;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 LGSYSRRRPFSTSTGR 18
||| ||| ||| ||| |||
DB 105 ISFARFRVSVSTGR 118

RESULT 38
D96597
hypothetical protein T5A14.9 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 12-Jul-2004
A;Accession: D96597
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D96597
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <STO>
A;Cross-references: UNIPROT:Q9SAV3; UNIPARC:UPI00000A71A3; GB:AE005173; NID:g4204270; PII
C;Genetics:
A;Gene: T5A14.9
A;Map position: 1
C;Superfamily: pyruvate dehydrogenase, E1 component, beta subunit

Query Match 44.0%; Score 40; DB 2; Length 352;
Best Local Similarity 57.1%; Pred. No. 61;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 LGSYSRRRPFSTSTGR 18
||| ||| ||| ||| |||
DB 17 LSHGARRVSTETGK 30

RESULT 39
C85022
hypothetical protein AT4g01730 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
A;Accession: C85022
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: C85022
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-499 <STO>
A;Cross-references: UNIPROT:Q9M115; UNIPARC:UPI000009EC49; GB:NC_001268; NID:g7268216; P:
C;Genetics:
A;Gene: AT4g01730
A;Map position: 4

Query Match 44.0%; Score 40; DB 2; Length 499;
Best Local Similarity 64.3%; Pred. No. 85;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 GRLSYRRRPFSTST 16
||| ||| ||| ||| |||
DB 437 GRFSSPRRRFSGSS 450

RESULT 40
O4CHC7
steroid 17alpha-monooxygenase (EC 1.14.99.9) cytochrome P450 17 - chicken
N;Alternate names: cytochrome P450(c17); steroid 17alpha-hydroxylase
C;Species: Gallus gallus (chicken)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: J070318
R;Ono, H.; Iwasaki, M.; Sakamoto, N.; Mizuno, S.
Gene 66, 77-85, 1988
A;Title: cDNA cloning and sequence analysis of a chicken gene expressed during the gonad
A;Reference number: J070318; MUID:88323730; PMID:3047010
A;Accession: J070318
A;Molecule type: mRNA
A;Residues: 1-508 <ONO>
A;Cross-references: UNIPROT:P12394; UNIPARC:UPI0000128307; GR:M21406; NID:g212492; PIDN:
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: chromoprotein; heme; iron; metalloprotein; monooxygenase; ovary; oxidoreduct
F;302-467/Domain: cytochrome P450 homology <CYP>
F;445/Binding site: heme iron (Cys) (axial ligand) #status predicted
Query Match 44.0%; Score 40; DB 1; Length 508;
Best Local Similarity 60.0%; Pred. No. 86;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 4 RLSYSRRRSTSTGR 18
Db 18 RLSYSQGPTGTGTCR 32

Search completed: May 21, 2006, 00:24:47
Job time : 40 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 21, 2006, 00:15:45 ; Search time 295 Seconds
(without alignments)
56.442 Million cell updates/sec

Title: US-09-857-000a-11

Perfect score: 91

Sequence: 1 RGRLSYSRRRSTSTGR 18

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot_7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	67.0	149	1 PG1_PIG	P212194 sus scrofa
2	56	61.5	109	2 Q70V15_9VIRU	Q70V15 daphne viru
3	55	60.4	147	1 PG2_PIG	P32195 sus scrofa
4	54	59.3	149	1 PG3_PIG	P32196 sus scrofa
5	54	59.3	149	1 PG5_PIG	P49934 sus scrofa
6	52	57.1	173	2 Q9ETA8_COREQ	Q9ETA8 corynebacte
7	51	56.0	108	2 Q80P41_9VIRU	Q80P41 narcissus c
8	50	54.9	109	2 Q5GR18_9VIRU	Q5GR18 daphne viru
9	49	53.8	476	1 GATB_LACJO	P61344 lactobacill
10	48	52.7	102	2 Q80P37_9VIRU	Q80P37 narcissus c
11	48	52.7	1062	2 Q4WPD8_ASPTU	Q4WPD8 aspergillus
12	47	51.6	91	2 Q68IP8_9VIRU	Q68IP8 potato viru
13	47	51.6	92	2 Q38024_9VIRU	Q38024 potato viru
14	47	51.6	93	2 Q73508_9VIRU	Q73508 potato viru
15	47	51.6	93	2 Q73509_9VIRU	Q73509 potato viru
16	47	51.6	93	2 Q73512_9VIRU	Q73512 potato viru
17	47	51.6	93	2 Q73514_9VIRU	Q73514 potato viru
18	47	51.6	93	2 Q73527_9VIRU	Q73527 potato viru
19	47	51.6	93	2 Q73529_9VIRU	Q73529 potato viru
20	47	51.6	93	2 Q73531_9VIRU	Q73531 potato viru
21	47	51.6	93	2 Q93139_9VIRU	Q93139 potato viru
22	47	51.6	94	2 Q73525_9VIRU	Q73525 potato viru
23	47	51.6	94	2 Q4A305_9VIRU	Q4A305 potato viru
24	47	51.6	94	2 Q4U6V1_9VIRU	Q4U6V1 potato viru
25	47	51.6	94	2 Q6R5K2_9VIRU	Q6R5K2 potato viru
26	47	51.6	94	2 Q86541_9VIRU	Q86541 potato viru
27	47	51.6	391	2 Q3MVD3_9DELT	Q3MVD3 syntrophoba
28	46.5	51.1	699	2 Q55Q95_CRYNE	Q55Q95 cryptococcu
29	46.5	51.1	699	2 Q5KFX2_CRYNE	Q5KFX2 cryptococcu
30	46	50.5	94	2 Q41486_9VIRU	Q41486 potato viru
31	46	50.5	233	2 Q3FAL7_9BURK	Q3FAL7 burkholderi

ALIGNMENTS

32	46	50.5	236	2	O16689_CABEL	O16689 caenorhabdi
33	45.5	50.0	288	2	Q7PPF7_MACRU	Q7PPF7 anopheles g
34	45	49.5	59	1	HSP1_MACRU	P42142 macropus ru
35	45	49.5	60	1	HSP1_CABFU	P42131 caenolestes
36	45	49.5	60	1	HSP1_DASHA	P67834 dasyurus ha
37	45	49.5	60	1	HSP1_DENGO	P67838 dendrolagus
38	45	49.5	60	1	HSP1_MACAG	P42137 macropus ag
39	45	49.5	60	1	HSP1_MACPA	Q9GLG9 macropus pa
40	45	49.5	60	1	HSP1_ONCFR	Q9GLG3 onychogalea
41	45	49.5	60	1	HSP1_ONYUN	P67839 onychogalea
42	45	49.5	60	1	HSP1_POTLO	Q9GL98 potorous lo
43	45	49.5	60	1	HSP1_SETRB	P67840 setonix bra
44	45	49.5	61	1	HSP1_ANTLA	O67845 antechinomy
45	45	49.5	61	1	HSP1_BETPE	Q9GLQ0 bettongia p
46	45	49.5	61	1	HSP1_DASAL	P67851 dasyurus al
47	45	49.5	61	1	HSP1_DASGE	P67850 dasyurus ge
48	45	49.5	61	1	HSP1_DASMA	P62485 dasyurus ma
49	45	49.5	61	1	HSP1_DASSP	P67849 dasyurus sp
50	45	49.5	61	1	HSP1_DASVI	P67835 dasyurus vi
51	45	49.5	61	1	HSP1_LAGFI	Q86696 lagostrophu
52	45	49.5	61	1	HSP1_NEOLO	P67852 neophascoga
53	45	49.5	61	1	HSP1_PARBI	O18758 parantechin
54	45	49.5	61	1	HSP1_PHADO	P67853 phascosor
55	45	49.5	61	1	HSP1_SARHA	P62486 sarcophilus
56	45	49.5	61	1	HSP1_SMILO	Q9TUC2 sminthopsis
57	45	49.5	62	1	HSP1_ANTFL	Q71V18 antechinus
58	45	49.5	62	1	HSP1_ANTBE	Q71V20 antechinus
59	45	49.5	62	1	HSP1_ANTGO	Q71V17 antechinus
60	45	49.5	62	1	HSP1_ANTHA	Q71V13 antechinus
61	45	49.5	62	1	HSP1_ANTLE	Q71V16 antechinus
62	45	49.5	62	1	HSP1_ANTMI	Q71V14 antechinus
63	45	49.5	62	1	HSP1_ANTNI	Q71V19 antechinus
64	45	49.5	62	1	HSP1_ANTNA	Q71V12 antechinus
65	45	49.5	62	1	HSP1_ANTST	P42129 antechinus
66	45	49.5	62	1	HSP1_ANTSW	Q71V22 antechinus
67	45	49.5	62	1	HSP1_DASBY	Q71V97 dasyuroides
68	45	49.5	62	1	HSP1_DASCR	Q71V98 dasyercus
69	45	49.5	62	1	HSP1_DASRO	P67830 dasykaluta
70	45	49.5	62	1	HSP1_MURLO	P67848 murexia lon
71	45	49.5	62	1	HSP1_MURRO	Q71V11 murexia rot
72	45	49.5	62	1	HSP1_MYOME	Q71VH0 myoictis me
73	45	49.5	62	1	HSP1_MYOMA	Q71V99 myoictis wa
74	45	49.5	62	1	HSP1_MYRFA	P67845 myrmecobius
75	45	49.5	62	1	HSP1_NINRI	Q71V97 ningau rid
76	45	49.5	62	1	HSP1_NINTI	Q71V95 ningau tim
77	45	49.5	62	1	HSP1_NINTV	Q71V96 ningau yvo
78	45	49.5	62	1	HSP1_PARAP	P67831 parantechin
79	45	49.5	62	1	HSP1_PHACL	Q71V10 phascogale
80	45	49.5	62	1	HSP1_PHATA	P67847 phascogale
81	45	49.5	62	1	HSP1_PLAMM	Q71V94 planigale m
82	45	49.5	62	1	HSP1_PSEMD	P67832 pseudantech
83	45	49.5	62	1	HSP1_PSENI	Q71V95 pseudantech
84	45	49.5	62	1	HSP1_PSEWO	Q71V94 pseudantech
85	45	49.5	62	1	HSP1_SMIAT	Q71V99 sminthopsis
86	45	49.5	62	1	HSP1_SMIAR	Q71V98 sminthopsis
87	45	49.5	62	1	HSP1_SMIIB	Q9TUC4 sminthopsis
88	45	49.5	62	1	HSP1_SMICR	P67844 sminthopsis
89	45	49.5	62	1	HSP1_SMIDL	Q71V97 sminthopsis
90	45	49.5	62	1	HSP1_SMIDO	Q71V96 sminthopsis
91	45	49.5	62	1	HSP1_SMIGA	Q71V94 sminthopsis
92	45	49.5	62	1	HSP1_SMIGI	Q71V95 sminthopsis
93	45	49.5	62	1	HSP1_SMIHI	Q71V93 sminthopsis
94	45	49.5	62	1	HSP1_SMIIE	Q71V92 sminthopsis
95	45	49.5	62	1	HSP1_SMIWA	Q71V98 sminthopsis
96	45	49.5	62	1	HSP1_SMIWA	Q71V99 sminthopsis
97	45	49.5	62	1	HSP1_SMIWO	Q71V91 sminthopsis
98	45	49.5	62	1	HSP1_SMIWS	Q71V90 sminthopsis
99	45	49.5	62	1	HSP1_SMIWI	Q71V99 sminthopsis
100	45	49.5	62	1	HSP1_SMIYO	Q71V98 sminthopsis

RESULT 1
PGL_PIG STANDARD; PRT; 149 AA.
AC P32194;
DT 01-OCT-1993, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 2.
DT 07-FEB-2006, entry version 49.
DE Protegrin-1 precursor (PG-1) (Neutrophil peptide 1).
GN #Name=PG1;
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bone marrow;
RX MEDLINE=94283613; PubMed=8013647; DOI=10.1016/0014-5793(94)00493-5;
RA Zhao C., Liu L., Lehrer R.I.;
RT "Identification of a new member of the protegrin family by cDNA
cloning.";
RL FEBS Lett. 346:285-288(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Red Duroc;
RX MEDLINE=95354835; PubMed=7628604; DOI=10.1016/0014-5793(95)00633-K;
RA Zhao C., Ganz T., Lehrer R.I.;
RT "The structure of porcine protegrin genes.";
RL FEBS Lett. 368:197-202(1995).
RN [3]
RP PROTEIN SEQUENCE OF 131-148.
RC TISSUE=Leukocyte; PubMed=8335113; DOI=10.1016/0014-5793(93)80175-T;
RX MEDLINE=93327946; PubMed=8335113; DOI=10.1016/0014-5793(93)80175-T;
RA Kokryakov V.N., Harwig S.S.L., Fanyutich E.A., Shevchenko A.A.,
RA Alekhina G.M., Shamova O.V., Korneva H.A., Lehrer R.I.;
RT "Protegrins: leukocyte antimicrobial peptides that combine features of
corticostatic defensins and tachyplesins.";
RL FEBS Lett. 327:231-236(1993).
RN [4]
RP PROTEIN SEQUENCE OF 131-148.
RC TISSUE=Neutrophil;
RX MEDLINE=93387466; PubMed=8375505; DOI=10.1016/0014-5793(93)80900-F;
RA Margorodskaya O.A., Shevchenko A.A., Abdalla K.O.M.A.,
RA Chernushevich I.V., Egorov T.A., Musoliamov A.X., Kokryakov V.N.,
RA Shamova O.V.;
RT "Primary structure of three cationic peptides from porcine
neutrophils. Sequence determination by the combined usage of
electrospray ionization mass spectrometry and Edman degradation.";
RL FEBS Lett. 330:339-342(1993).
RN [5]
RP STRUCTURE BY NMR OF PROTEGRIN 1.
RX MEDLINE=96235220; PubMed=8647100;
RA Amelase A., Mangoni M., Roumestand C., Chiche L., Despaux E.,
RA Grassy G., Calas B., Chavanier A.;
RT "Synthesis and solution structure of the antimicrobial peptide
protegrin-1.";
RL Eur. J. Biochem. 237:575-583(1996).
RN [6]
RP STRUCTURE BY NMR OF PROTEGRIN 1.
RX MEDLINE=97113279; PubMed=8807886; DOI=10.1016/S1074-5521(96)90145-3;
RA Fahrner R.L., Dieckmann T., Harwig S.S., Lehrer R.I., Eisenberg D.,
RA Feigon J.;
RT "Solution structure of protegrin-1, a broad-spectrum antimicrobial
peptide from porcine leukocytes.";
RL Chem. Biol. 3:543-550(1996).
CC CC -1- FUNCTION: Microbicidal activity. Active against E.coli, Listeria
monocytogenes and C.albicans in vitro.
CC CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC CC -1- SIMILARITY: Belongs to the cathelicidin family.
CC
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CC
DR EMBL; X79868; CAA56251.1; -; mRNA.
DR EMBL; X84094; CAA58890.1; -; Genomic_DNA.
DR FIR; S66284; S57607.
DR PDB; 1PG1; NMR; Q=131-148.
DR SNR; P32194; 30-130.
DR InterPro; IPR001894; Cathelicidin.
DR PANTHER; PTHR10206; Cathelicidin; 1.
DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS 1; 1.
DR PROSITE; PS00947; CATHELICIDINS 2; 1.
KW 3D-structure; Amidation; Antibiotic; Antimicrobial;
KW Direct protein sequencing; Pyrrolidone carboxylic acid; Signal.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 130 /FTid=PRO_0000004744;
FT PEPTIDE 131 148 Protegrin-1.
FT /FTid=PRO_0000004745.
FT MOD_RES 30 30 Pyrrolidone carboxylic acid (By
FT similarity).
FT MOD_RES 148 148 Arginine amide (G-149 provides amide
FT group).
FT DISULFID 85 96 By similarity.
FT DISULFID 107 124 By similarity.
FT DISULFID 136 145 By similarity.
FT DISULFID 138 143
FT STRAND 133 139
FT TURN 140 141
FT STRAND 142 147
SQ SEQUENCE 149 AA; 16677 MW; 6EFBA98429CD6EC4 CRC64;
Query Match 67.0%; Score 61; DB 1; Length 149;
Best Local Similarity 66.7%; Pred.No. 0.031;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 RGGRLSYRRRRFSTGTR 18
|||||
DB 131 RGGRLCYCRRFCVCVGR 148
RESULT 2
Q70V15_9VIRU
ID Q70V15_9VIRU PRELIMINARY; PRT; 109 AA.
AC Q70V15;
DT 03-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Hypothetical 12K protein.
OS Daphne virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=216614;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Kr2;
RX MEDLINE=22897970; PubMed=14551815; DOI=10.1007/s00705-003-0161-2;
RA Lee B.Y., Choi S.H., Ryu K.H.;
RT "Characterization of the 3'-terminal nucleotide sequence of two Korean
isolates of Daphne virus S support its placement as a distinct species
of the genus Carlavirus.";
RL Arch. Virol. 148:1915-1924(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Kr2;
RA Ryu K.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; AJ535085; CAD59393.1; -; Genomic RNA.
CC GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO: 0006355; P: regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR002568; Carla_Bd.
 DR Pfam: PF01623; Carla_C1; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 109 AA; 12328 MW; BC0338DEB44CED84 CRC64;
 Query Match 61.5%; Score 56; DB 2; Length 109;
 Best Local Similarity 64.7%; Pred. No. 0.16;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 GGRLSYRRRPFSTSTGR 18
 |||||:|:|:|:|:|
 Db 42 GGRSSYARKRATSIQR 58
 |||||:|:|:|:|:|
 RESULT 3
 PG2_PIG ID PG2_PIG STANDARD; PRT; 147 AA.
 AC P32195;
 DT 01-OCT-1993, integrated into UniProtKB/Swiss-Prot.
 DT 01-OCT-1996, sequence version 2.
 DT 07-FEB-2006, entry version 43.
 DE Protegrin-2 precursor (PG-2).
 GN Name=PG2;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Bone marrow;
 RA MEDLINE=94071898; PubMed=8250892;
 RX Storicci P., Zanetti M.;
 RT "A novel cDNA sequence encoding a pig leukocyte antimicrobial peptide
 with a cathelin-like pro-sequence.";
 RT Biochem. Biophys. Res. Commun. 196:1363-1368(1993).
 RN [2]
 RP PROTEIN SEQUENCE OF 131-146.
 RC TISSUE=Leukocyte;
 RX MEDLINE=93327946; PubMed=8335113; DOI=10.1016/0014-5793(93)80175-T;
 RA Kokryakov V.N., Harwig S.S.L., Panyutich E.A., Shevchenko A.A.,
 RA Alekhina G.M., Shamova O.V., Korneva H.A., Lehrer R.I.;
 RT "Protegrins: leukocyte antimicrobial peptides that combine features of
 corticostatic defensins and tachyplesins.";
 RL FEBS Lett. 327:231-236(1993).
 CC -1- FUNCTION: Microbicidal activity. Active against E.coli, Listeria
 CC monocytes and C.albicans, in vitro.
 CC -1- SUBCELLULAR LOCATION: Secreted protein.
 CC -1- SIMILARITY: Belongs to the cathelicidin family.
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 CC -----
 DR EMBL; L24745; AAA31061.1; -; mRNA.
 DR PIR; JN0900; JN0900.
 DR HSSP; P32196; 1LXE.
 DR SMR; P32195; 30-130.
 DR InterPro: IPR001894; Cathelicidin.
 DR PANTHER; PTHR10206; Cathelicidins; 1.
 DR Pfam; PF00666; Cathelicidins; 1.
 DR ProDom; PD001838; Cathelicidins; 1.
 DR PROSITE; PS00946; CATHELICIDINS 1; 1.
 DR PROSITE; PS00947; CATHELICIDINS 2; 1.
 KW Amidation; Antibiotic; Antimicrobial; Direct protein sequencing;
 KW Pyroglutamate; Pyroglutamic acid; Signal.
 FT SIGNAL 1 29 Potential.
 FT PROPEP 30 130
 /FTid=PRO_0000004746.
 FT PEPTIDE 131 146
 /FTid=PRO_0000004747.
 FT MOD_RES 30 30 Pyroglutamate carboxylic acid (By
 similarity).

PT MOD_RES 146 146 Valine amide (G-147 provides amide
 group).
 FT DISULFID 85 96 By similarity.
 FT DISULFID 107 124 By similarity.
 FT DISULFID 136 145 By similarity.
 FT DISULFID 138 143 By similarity.
 SQ SEQUENCE 147 AA; 16478 MW; 698429DFEFC40466 CRC64;
 Query Match 60.4%; Score 55; DB 1; Length 147;
 Best Local Similarity 64.7%; Pred. No. 0.34;
 Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 RGRLSYRRRPFSTSTG 17
 |||||:|:|:|:|:|
 Db 131 RGRLCYCRRRFCICVG 147
 |||||:|:|:|:|:|
 RESULT 4
 PG3_PIG ID PG3_PIG STANDARD; PRT; 149 AA.
 AC P32196;
 DT 01-OCT-1993, integrated into UniProtKB/Swiss-Prot.
 DT 01-OCT-1996, sequence version 2.
 DT 07-FEB-2006, entry version 47.
 DE Protegrin-3 precursor (PG-3).
 GN Name=PG3;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Bone marrow;
 RX MEDLINE=94283613; PubMed=8013647; DOI=10.1016/0014-5793(94)00493-5;
 RA Zhao C., Liu L., Lehrer R.I.;
 RT "Identification of a new member of the protegrin family by cDNA
 cloning.";
 RL FEBS Lett. 346:285-288(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Red Duroc;
 RX MEDLINE=95354835; PubMed=7628604; DOI=10.1016/0014-5793(95)00633-K;
 RA Zhao C., Ganz T., Lehrer R.I.;
 RT "The structure of porcine protegrin genes.";
 RL FEBS Lett. 368:197-202(1995).
 RN [3]
 RP PROTEIN SEQUENCE OF 131-148.
 RC TISSUE=Leukocyte;
 RX MEDLINE=93327946; PubMed=8335113; DOI=10.1016/0014-5793(93)80175-T;
 RA Kokryakov V.N., Harwig S.S.L., Panyutich E.A., Shevchenko A.A.,
 RA Alekhina G.M., Shamova O.V., Korneva H.A., Lehrer R.I.;
 RT "Protegrins: leukocyte antimicrobial peptides that combine features of
 corticostatic defensins and tachyplesins.";
 RL FEBS Lett. 327:231-236(1993).
 CC -1- FUNCTION: Microbicidal activity. Active against E.coli, Listeria
 CC monocytes and C.albicans, in vitro.
 CC -1- SUBCELLULAR LOCATION: Secreted protein.
 CC -1- SIMILARITY: Belongs to the cathelicidin family.
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 CC -----
 DR EMBL; X83267; CAA58240.1; -; mRNA.
 DR EMBL; X84095; CAA58891.1; -; Genomic_DNA.
 DR PIR; S66285; A53895.
 DR PDB; 1LXI; X-ray; A=30-130.
 DR PDB; 1LXE; X-ray; A=30-130.
 DR PDB; 1PFP; X-ray; A=30-130.
 DR InterPro: IPR001894; Cathelicidin.
 DR PANTHER; PTHR10206; Cathelicidins; 1.
 DR Pfam; PF00666; Cathelicidins; 1.
 DR ProDom; PD001838; Cathelicidins; 1.
 DR PROSITE; PS00946; CATHELICIDINS 1; 1.
 DR PROSITE; PS00947; CATHELICIDINS 2; 1.
 KW Amidation; Antibiotic; Antimicrobial; Direct protein sequencing;
 KW Pyroglutamate; Pyroglutamic acid; Signal.
 FT SIGNAL 1 29 Potential.
 FT PROPEP 30 130
 /FTid=PRO_0000004746.
 FT PEPTIDE 131 146
 /FTid=PRO_0000004747.
 FT MOD_RES 30 30 Pyroglutamate carboxylic acid (By
 similarity).

DR PROSITE; PS00946; CATHELICIDINS 1; 1.
DR PROSITE; PS00947; CATHELICIDINS 2; 1.
KW 3D-structure; Amidation; Antibiotic; Antimicrobial; Pyrrrolidone carboxylic acid; Signal.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 130
FT PEPTIDE 131 148 /FTID=PRO_0000004748.
FT FTID=PRO_0000004749.
FT MOD_RES 30 30 Pyrrrolidone carboxylic acid (By
FT MOD_RES 148 148 Arginine amide (G-149 provides amide
FT DISULFID 85 96 By similarity.
FT DISULFID 107 124 By similarity.
FT DISULFID 136 145 By similarity.
FT DISULFID 138 143 By similarity.
FT HELIX 32 48
FT STRAND 51 60
FT STRAND 74 88
FT STRAND 91 91
FT STRAND 93 95
FT STRAND 96 96
FT STRAND 98 98
FT TURN 100 101
FT STRAND 104 111
FT STRAND 121 126
SQ SEQUENCE 149 AA; 16578 MW; 6F4BA98429CD6ED4 CRC64;

Query Match 59.3%; Score 54; DB 1; Length 149;

Best Local Similarity 61.1%; Pred. No. 0.52; Mismatches 0; Indels 7; Gaps 0;

QY 1 RGRLSYSRRRPFSTSTGR 18
||| |||||
Db 131 RGGGLCYCRRRPFVCVGR 148

RESULT 5

PG5_PIG STANDARD; PRT; 149 AA.
AC P49934;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 38.
DE Protegrin-5 precursor (PG-5).
GN Name=PG5;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC MEDLINE=95354835; PubMed=7628604; DOI=10.1016/0014-5793(95)00633-K;
RX Zhao C., Ganz T., Lehrer R.I.;
RT "The structure of porcine protegrin genes.";
RL FEBS Lett. 368:197-202(1995).
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- SIMILARITY: Belongs to the cathelicidin family.
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; X84096; CAA58892.1; -; Genomic_DNA.
DR PIR; S66283; S57609.
DR HSP; P32196; ILXE.
DR SMR; P49934; 30-130.
DR InterPro; IPR001894; Cathelicidin.
DR PANTHER; PTHR10206; Cathelicidin; 1.
DR Pfam; PF00666; Cathelicidins; 1.

DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS 1; 1.
DR PROSITE; PS00947; CATHELICIDINS 2; 1.
KW Amidation; Antibiotic; Antimicrobial; Pyrrrolidone carboxylic acid; Signal.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 130 /FTID=PRO_0000004752.
FT PEPTIDE 131 148 Protegrin-5
FT FTID=PRO_0000004753.
FT MOD_RES 30 30 Pyrrrolidone carboxylic acid (By
FT MOD_RES 148 148 Arginine amide (G-149 provides amide
FT DISULFID 85 96 By similarity.
FT DISULFID 107 124 By similarity.
FT DISULFID 136 145 By similarity.
FT DISULFID 138 143 By similarity.
SQ SEQUENCE 149 AA; 16604 MW; 6CC7262429CD6B64 CRC64;

Query Match 59.3%; Score 54; DB 1; Length 149;

Best Local Similarity 61.1%; Pred. No. 0.52; Mismatches 0; Indels 7; Gaps 0;

QY 1 RGRLSYSRRRPFSTSTGR 18
||| |||||
Db 131 RGRLCYCRPRFCVGR 148

RESULT 6

O9ETA8_COREQ PRELIMINARY; PRT; 173 AA.
AC O9ETA8;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein orf58.
GN Name=orf58;
OS Corynebacterium equi (Rhodococcus equi).
OG Plasmid pREAT701 (p33701), and Plasmid virulence plasmid.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=43767;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=103, and ATCC33701; PLASMID=pREAT701 (p33701), and virulence
RC Plasmid;
RX MEDLINE=20536428; PubMed=11083803;
RX DOI=10.1128/IAI.68.12.6840-6847.2000;
RA Takai S., Hines S.A., Sekizaki T., Nicholson V.M., Alperin D.A.,
RA Osaki M., Takamatsu D., Nakamura M., Suzuki K., Ogino N., Kakuda T.,
RA Dan H., Prescott J.F.;
RT "DNA sequence and comparison of virulence plasmids from Rhodococcus
RT equi ATCC 33701 and 103.";
RL Infect. Immun. 68:6840-6847(2000).
CC
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CC
CC EMBL; AP001204; BAB15667.1; -; Genomic DNA.
DR EMBL; AF116907; AAG21761.1; -; Genomic_DNA.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 173 AA; 18852 MW; F18A637BCA404053 CRC64;

Query Match 57.1%; Score 52; DB 2; Length 173;

Best Local Similarity 52.9%; Pred. No. 1.4; Mismatches 9; Conservative 4; Indels 4; Gaps 0;

QY 2 GGRLSYSRRRPFSTSTGR 18
||| |||||
Db 142 GGRISVASLRYTDTGR 158

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SQ  SEQUENCE      109 AA; 12364 MW;  2AE245589FBE5E10 CRC64;
Query Match          54.9%; Score 50; DB 2; Length 109;
Best Local Similarity 58.8%; Pred. No. 1.8;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps

QY  2 GGRLSYRRRFRSTSTGR 18
    |||:|:|:|:|
DB  42 GGRSSYARRKRALSTGR 58

RESULT 9
GATB_LACJO
ID      GATB_LACJO      STANDARD;      PRT;      476 AA.
AC      P61344;
DT      10-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT      10-MAY-2004, sequence version 1.
DT      07-MAR-2006, entry version 14.
DE      Aspartyl-glutamyl-tRNA(Asn/Gln) amidotransferase subunit B
DE      (EC 6.3.5.-) (Asp/Glu-ADT subunit B).
GN      Name=gatB; OrderedLocuNames=LJ1716;
OS      Lactobacillus johnsonii.
OC      Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC      Lactobacillus.
OX      NCBI_TaxID=33959;
OX      [1]
RN      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP      STRAIN=NCC 533;
RC      PubMed=14983040; DOI=10.1073/pnas.0307327101;
RX      Fridmore R.D., Berger B., Desiere F., Villanova D., Barretto C.,
RA      Pitket A.-C., Zwaalen M.-C., Rouvet M., Altermann E., Barrangou R.,
RA      Mollet B., Mercenier A., Kleenhammer T., Arigoni F., Schell M.A.;
RT      "The genome sequence of the probiotic intestinal bacterium
RT      Lactobacillus johnsonii NCC 533 ";
RL      Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
CC      -I- FUNCTION: Allows the formation of correctly charged Asn-tRNA(Asn)
CC      or Gln-tRNA(Gln) through the transamidation of misacylated Asp-
CC      tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both
CC      of asparaginyl-tRNA or glutamyl-tRNA synthetases. The reaction
CC      takes place in the presence of glutamine and ATP through an
CC      activated phospho-Asp-tRNA(Asn) or phospho-Glu-tRNA(Gln) (By
CC      similarity).
CC      -I- CATALYTIC ACTIVITY: ATP + L-glutamyl-tRNA(Gln) + L-glutamine = ADP
CC      + phosphate + L-glutamyl-tRNA(Gln) + L-glutamate.
CC      -I- CATALYTIC ACTIVITY: ATP + L-aspartyl-tRNA(Asn) + L-glutamine = ADP
CC      + phosphate + L-asparaginyl-tRNA(Asn) + L-glutamate.
CC      -I- SUBUNIT: Heterotrimer of A, B and C subunits (By similarity).
CC      -I- SIMILARITY: Belongs to the gatB/gatC family. GatB subfamily.
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CC      -----
CC      EMBL; AE017198; AAC09487.1; ; Genomic_DNA.
DR      GenomeReviews; AE017198 GR; LJ1716.
DR      BioCyc; LJOH257314:LJ1716-MONOMER; -.
DR      HAMAP; MF_00121; -.
DR      InterPro; IPR004413; GatB.
DR      InterPro; IPR006107; GatB_central.
DR      InterPro; IPR006075; GatB_N.
DR      InterPro; IPR003789; GatB_Yqey.
DR      PANTHER; PTHR11659; GatB; 1.
DR      Pfam; PF01162; GatB; 1.
DR      Pfam; PF02934; GatB_N; 1.
DR      Pfam; PF04637; GatB_Yqey; 1.
DR      TIGRFAMs; TIGR001033; gatB; 1.
DR      PROSITE; PS01234; GatB; 1.
DR      Complete proteome; Ligase; Protein biosynthesis.
KW      Aspartyl-glutamyl-tRNA(Asn/Gln)
FT      amidotransferase subunit B.
FT      /FTid=PRO_0000148796.
SQ  SEQUENCE      476 AA; 53804 MW;  5A13505687A9A014 CRC64;
Query Match          53.8%; Score 49; DB 1; Length 476;

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Best Local Similarity 52.9%; Pred. No. 15;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFRSTGTGR 18
    |||: ||||| :||:
Db 239 GGRVQLSTRFRDEATGK 255

RESULT 10
Q80P37_9VIRU
ID Q80P37_9VIRU PRELIMINARY; PRT; 102 AA.
AC Q80P37;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DE Nucleic acid binding protein.
DE Nucleic acid binding protein.
OS Narcissus common latent virus.
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=160844;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP Chen J., Chen J., Langeveld S.A., Derks A.F.L.M., Adams M.J.;
RA "Molecular characterization of carla- and potyvirus from Narcissus
RT in China.";
RL J. Phytopathol. 151:26-29(2003).
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CC -----
DR EMBL; AJ311376; CAC85389.1; -; Genomic RNA.
DR GO; GO:0003576; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
SQ SEQUENCE 102 AA; 11446 MW; 929B1615860484CC CRC64;

Query Match 52.7%; Score 48; DB 2; Length 102;
Best Local Similarity 52.9%; Pred. No. 3.7;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFRSTGTGR 18
    |||: ||||| :||:
Db 40 GGRSSYRRRRRAANIGR 56

RESULT 11
Q4W9D8_ASPFU
ID Q4W9D8_ASPFU PRELIMINARY; PRT; 1062 AA.
AC Q4W9D8;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-MAR-2006, entry version 6.
DE Von Willebrand domain protein.
GN CRPFName-Afu4901160;
OS Aspergillus fumigatus (Sartorya fumigatus).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5085;
RN [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Af293 / CBS 101355 / FGSC A1100;
RX PubMed=16372009; DOI=10.1038/nature04332;
RA Nierman W.C., Pain A., Anderson M.J., Wortman J.R., Kim H.S.,
RA Arroyo J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.W.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N.D., Feldblyum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.J.,
RA Haas H., Harris D.B., Horiuchi H., Huang J., Humphray S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Konzack S.,
RA Kulkarni R., Kumagai T., Lafont A., Latge J.-P., Li W., Lord A.,
RA Lu C., Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,
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RA Monod M., Mouyna I., Mulligan S., Murphy L.D., O'Neil S., Paulsen I.,
RA Penalba M.A., Perteu M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitsch E., Rawlins N., Rajandream M.A., Reichard U.,
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Roming C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala J.R., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J.R., Yu J.-H., Fraser C.M., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B.G., Denning D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus.";
RL Nature 438:1151-1156(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAHP01000017; EAL84303.1; -; Genomic_DNA.
DR InterPro; IPR006587; VIT.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWEFA; 1.
KW Complete proteome.
SQ SEQUENCE 1062 AA; 117219 MW; EF2F3AF2B1B5FB4B CRC64;

Query Match 52.7%; Score 48; DB 2; Length 1062;
Best Local Similarity 61.1%; Pred. No. 55;
Matches 11; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 RGRLSYRRRFRSTGTGR 18
    |||: ||||| :||:
Db 719 RGLLSYPRREFLASTSR 736

RESULT 12
Q68IP8_9VIRU
ID Q68IP8_9VIRU PRELIMINARY; PRT; 91 AA.
AC Q68IP8;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE 11K protein.
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP Lang Q., Chen J., Du Z.;
RA "Molecular Identification of PVS in Hangzhou.";
RT Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY687337; AAT97709.1; -; Genomic RNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
SQ SEQUENCE 91 AA; 10264 MW; 02A0F98659B9812D CRC64;

Query Match 51.6%; Score 47; DB 2; Length 91;
Best Local Similarity 52.9%; Pred. No. 4.8;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFRSTGTGR 18
    |||: ||||| :||:
Db 38 GGRSTYRKRRRSIGR 54
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RESULT 13
O38024 9VIRU
ID O38024 9VIRU PRELIMINARY; PRT; 92 AA.
AC O38024;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Hypothetical protein.
OS Potato virus M.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12167;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Idaho;
RA Cavilser T.D.; Corsini D.L.; Berger P.H.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
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EMBL; AF023877; AAB81273.1; -; Genomic RNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
KW Hypothetical protein.
SQ SEQUENCE 92 AA; 10319 MW; B0A9AC70B579A980 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 92;
Best Local Similarity 52.9%; Pred. No. 4.9;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 2 GGRLSYRRRFFSTGTGR 18
Db 40 GGRSKYARRRRRAIAGR 56

RESULT 14
O73508 9VIRU
ID O73508 9VIRU PRELIMINARY; PRT; 93 AA.
AC O73508;
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 11K protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Aschersleben;
RA Matousek J.; Schubert J.; Dedic P.; Ptacek J.;
RT "A broad variability of potato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse transcriptase-polymerase chain
RT reaction."
RL Can. J. Plant Pathol. 22:22-29(2000).
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EMBL; Y15613; CAA75702.1; -; Genomic DNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
FT NON_TER 93
SQ SEQUENCE 93 AA; 10521 MW; 2DA6E2925A8C475D CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 2 GGRLSYRRRFFSTGTGR 18
Db 38 GGRSTYARKRRARSIGR 54

RESULT 15
O73509 9VIRU
ID O73509 9VIRU PRELIMINARY; PRT; 93 AA.
AC O73509;
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 11K protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Aschersleben;
RA Matousek J.; Schubert J.; Dedic P.; Ptacek J.;
RT "A broad variability of potato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse transcriptase-polymerase chain
RT reaction."
RL Can. J. Plant Pathol. 22:22-29(2000).
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EMBL; Y15615; CAA75706.1; -; Genomic DNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
FT NON_TER 93
SQ SEQUENCE 93 AA; 10521 MW; 2DA6E2925A8C475D CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 2 GGRLSYRRRFFSTGTGR 18
Db 38 GGRSTYARKRRARSIGR 54

RESULT 16
O73512 9VIRU
ID O73512 9VIRU PRELIMINARY; PRT; 93 AA.
AC O73512;
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 11K protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Karla;
RA Matousek J.; Schubert J.; Dedic P.; Ptacek J.;
RT "A broad variability of potato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse transcriptase-polymerase chain
RT reaction."
RL Can. J. Plant Pathol. 22:22-29(2000).
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EMBL; Y15611; CAA75698.1; -; Genomic DNA.

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DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10538 MW; 11BD9C9997BB85 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFRSTSTGR 18
   |||:|:|:|:|:|
Db 38 GGRSTYARRRARSIGR 54

RESULT 17
O73514_9VIRU
ID O73514_9VIRU PRELIMINARY; PRT; 93 AA.
AC O73514_9VIRU
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 11k protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlaviruses.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Karla;
RA Matousek J., Schubert J., Dedic P., Ptacek J.;
RT "A broad variability of pot ato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse t ranscriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
EMBL; Y15612; CAA75700.1; -; Genomic DNA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10538 MW; 11BD9C9997BB85 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFRSTSTGR 18
   |||:|:|:|:|:|
Db 38 GGRSTYARRRARSIGR 54

RESULT 18
O73527_9VIRU
ID O73527_9VIRU PRELIMINARY; PRT; 93 AA.
AC O73527_9VIRU
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 11k protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlaviruses.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Vitava;
RA Matousek J., Schubert J., Dedic P., Ptacek J.;
RT "A broad variability of pot ato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse t ranscriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
EMBL; Y15612; CAA75700.1; -; Genomic DNA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10538 MW; 11BD9C9997BB85 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFRSTSTGR 18
   |||:|:~|:~|:~|:~|
Db 38 GGRSTYARRRARSIGR 54

RESULT 19
O73529_9VIRU
ID O73529_9VIRU PRELIMINARY; PRT; 93 AA.
AC O73529_9VIRU
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 11k protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlaviruses.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Vitava;
RA Matousek J., Schubert J., Dedic P., Ptacek J.;
RT "A broad variability of pot ato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse t ranscriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
EMBL; Y15616; CAA75708.1; -; Genomic DNA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10507 MW; AC2FE2A0F98645C9 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFRSTSTGR 18
   |||:~|:~|:~|:~|
Db 38 GGRSTYARRRARSIGR 54

RESULT 20
O73531_9VIRU
ID O73531_9VIRU PRELIMINARY; PRT; 93 AA.
AC O73531_9VIRU
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
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RT "A broad variability of pot ato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse t ranscriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
EMBL; Y15609; CAA75694.1; -; Genomic DNA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10333 MW; AB44F80C8018A5C9 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFRSTSTGR 18
   |||:~|:~|:~|:~|
Db 38 GGRSTYARRRARSIGR 54

RESULT 19
O73529_9VIRU
ID O73529_9VIRU PRELIMINARY; PRT; 93 AA.
AC O73529_9VIRU
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 11k protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlaviruses.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Vitava;
RA Matousek J., Schubert J., Dedic P., Ptacek J.;
RT "A broad variability of pot ato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse t ranscriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
EMBL; Y15616; CAA75708.1; -; Genomic DNA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10507 MW; AC2FE2A0F98645C9 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRFRSTSTGR 18
   |||:~|:~|:~|:~|
Db 38 GGRSTYARRRARSIGR 54

RESULT 20
O73531_9VIRU
ID O73531_9VIRU PRELIMINARY; PRT; 93 AA.
AC O73531_9VIRU
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
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DE 11k protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Vitava;
RA Matousek J., Schubert J., Dedic P., Ptacek J.;
RT "A broad variability of potato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse transcriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
DR EMBL; Y15610; CAA75696.1; -; Genomic DNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
FT NON TER .93
SQ SEQUENCE 93 AA; 10333 MW; AB44P80C8018A5C9 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRPFSTGTGR 18
   |||:|:|:|:|
Db 38 GGRSTYARKRRARSIGR 54

RESULT 21
O93139_9VIRU
ID O93139_9VIRU PRELIMINARY; PRT; 93 AA.
AC O93139
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE 11k protein (Fragment).
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Kobra;
RA Matousek J., Schubert J., Dedic P., Ptacek J.;
RT "A broad variability of potato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse transcriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
DR EMBL; Y15614; CAA75704.1; -; Genomic DNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
FT NON TER .93
SQ SEQUENCE 93 AA; 10566 MW; 11BD8D5D69865A75 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 93;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRPFSTGTGR 18
   |||:|:|:|:|
Db 38 GGRSTYARKRRARSIGR 54
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RESULT 22
O73525_9VIRU
ID O73525_9VIRU PRELIMINARY; PRT; 94 AA.
AC O73525
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 11k protein.
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Kobra;
RA Matousek J., Schubert J., Dedic P., Ptacek J.;
RT "A broad variability of potato virus S (PVS) revealed by analysis of
RT virus sequences amplified by reverse transcriptase-polymerase chain
RT reaction.";
RL Can. J. Plant Pathol. 22:22-29(2000).
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CC -----
DR EMBL; Y15625; CAA75721.1; -; Genomic DNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
SQ SEQUENCE 94 AA; 10666 MW; 5236BDFD583C830A CRC64;

Query Match 51.6%; Score 47; DB 2; Length 94;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGRLSYRRRPFSTGTGR 18
   |||:|:|:|:|
Db 38 GGRSTYARKRRARSIGR 54

RESULT 23
O4A3Q5_9VIRU
ID O4A3Q5_9VIRU PRELIMINARY; PRT; 94 AA.
AC O4A3Q5
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE 11k protein.
GN Names=11k;
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Leona;
RA Matousek J., Schubert J., Ptacek J., Kozlova P., Dedic P.;
RT "Molecular probing of PVS genome by immunocapture RT-PCR and by
RT thermodynamic analysis.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AJ863509; CAI06120.1; -; Genomic RNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
SQ SEQUENCE 94 AA; 10664 MW; A600348D6FCA8C44 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 94;
Best Local Similarity 52.9%; Pred. No. 5;
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Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 2 GGRLSYRRRFFSTSTGR 18
DB 38 GGRSTYARKRRARSIGR 54
||||:|:|:|:|

RESULT 24
Q4U6V1_9VIRU
ID Q4U6V1_9VIRU PRELIMINARY; PRT; 94 AA.
AC Q4U6V1;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE 11K protein.
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Andean;
RA Bystricka D., Lenz O., Mraz O., Piherova L., Kmoch S., Sip M.;
RT "Oligonucleotide-based microarray: a new improvement in microarray
detection of plant viruses.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; DQ000231; AAY33743.1; -; Genomic RNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
SQ SEQUENCE 94 AA; 10680 MW; 3E31A1FA37C4465A CRC64;

Query Match 51.6%; Score 47; DB 2; Length 94;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 2 GGRLSYRRRFFSTSTGR 18
DB 38 GGRSTYARKRRARSIGR 54
||||:|:|:|:|

RESULT 25
Q6R5K2_9VIRU
ID Q6R5K2_9VIRU PRELIMINARY; PRT; 94 AA.
AC Q6R5K2;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE 11K protein.
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Du Z.Y., Chen J.S.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY512653; AAS16473.1; -; Genomic RNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_b.
DR Pfam; PF01623; Carla_C4; 1.
SQ SEQUENCE 94 AA; 10708 MW; 9B61A1B3A5FF4D6 CRC64;

Query Match 51.6%; Score 47; DB 2; Length 94;
Best Local Similarity 52.9%; Pred. No. 5;
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Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 2 GGRLSYRRRFFSTSTGR 18
DB 38 GGRSTYARKRRARSIGR 54
||||:|:|:|:|

RESULT 26
Q86541_9VIRU
ID Q86541_9VIRU PRELIMINARY; PRT; 94 AA.
AC Q86541;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE 11 kDa protein (Polyprotein).
GN Name=11 kDa protein;
OS Potato virus S.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
OC Carlavirus.
OX NCBI_TaxID=12169;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93033173; PubMed=1413539;
RA Foster G.D., Mills P.R.;
RT "The 3'-nucleotide sequence of an ordinary strain of potato virus S.";
RL Virus Genes 6:213-220(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ordinary;
RA Bystricka D., Lenz O., Mraz O., Piherova L., Kmoch S., Sip M.;
RT "Oligonucleotide-based microarray: a new improvement in microarray
detection of plant viruses.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; S45593; AAB23462.1; -; Genomic RNA.
DR EMBL; DQ000232; AAY33744.1; -; Genomic RNA.
DR FIR; B48549; B48549.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_b.
DR Pfam; PF01623; Carla_C4; 1.
KW Polyprotein.
SQ SEQUENCE 94 AA; 10680 MW; 2241BD8D5D69865A CRC64;

Query Match 51.6%; Score 47; DB 2; Length 94;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 2 GGRLSYRRRFFSTSTGR 18
DB 38 GGRSTYARKRRARSIGR 54
||||:|:~|:|:|:|

RESULT 27
Q3MVD3_9DELT
ID Q3MVD3_9DELT PRELIMINARY; PRT; 391 AA.
AC Q3MVD3;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Alpha-methylacyl-CoA racemase (EC 5.1.99.4).
GN ORFNames=StumDRAFT_3519;
OS Synphobacterium fumaroxidans MFOB.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Syntrophobacterales;
OC Syntrophobacteraceae; Syntrophobacter.
OX NCBI_TaxID=335543;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MFOB;
RG US DOE Joint Genome Institute (JGI-PGF);
```

RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
 RA Hammon N., Israni S., Pittluck S., Richardson P.,
 RT "Sequencing of the draft genome and assembly of Syntriphobacter
 RL fumaroxidans MPOB.";
 RT Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=MPOB;
 RG US DOE Joint Genome Institute (JGI_ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of Syntriphobacter
 RL fumaroxidans MPOB.";
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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 CC -----
 CC EMBL; AJ270100.1; EAO18902.1; -; Genomic DNA.
 DR GO; GO:0008111; F:alpha-methylacyl-CoA racemase activity; IEA.
 DR GO; GO:0016853; F:Isomerase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR003673; CA1B_BA1P.
 DR Pfam; PF02515; CoA_transf_3; 1.
 KW Isomerases.
 SQ SEQUENCE 391 AA; 42948 MW; 7CE6207BECFC9F3D CRC64;
 Query Match 51.6%; Score 47; DB 2; Length 391;
 Best Local Similarity 64.7%; Pred. No. 26;
 Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 RGRGLYSRRRPFSTSTG 17
 Db 145 RSGVLSGGRAPTWG 161
 RESULT 28
 ID Q55Q95 CRYNE PRELIMINARY; PRT; 699 AA.
 AC Q55Q95;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Hypothetical protein.
 GN ORFNames=CNEF4420;
 OS Cryptococcus neoformans var. neoformans B-3501A.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 OX NCBI_TaxID=283643;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B-3501A;
 RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
 RA Wickes B.L., Fu J., Davis R.W.;
 RT "Cryptococcus neoformans serotype D sequencing.";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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 CC -----
 CC EMBL; AAFY01000032; EAL20116.1; -; Genomic DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 699 AA; 75973 MW; AFE9D14B9A2254EB CRC64;
 Query Match 51.1%; Score 46.5; DB 2; Length 699;
 Best Local Similarity 52.2%; Pred. No. 62;
 Matches 12; Conservative 0; Mismatches 6; Indels 5; Gaps 1;
 QY 1 RGRGLYSRRRPFSTSTG 18
 Db 291 RSGRSGYSDRSGSISRFGTSNGR 313
 RESULT 30
 ID Q41486 GVIRU PRELIMINARY; PRT; 94 AA.
 AC Q41486;
 DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
 DT 01-JAN-1998, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE 11k protein.
 OS Potato virus S.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
 OC Carlavirus.
 OX NCBI_TaxID=12169;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=S-RB;
 RA Joung Y.H.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
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QY 1 RGRGLYSRRRPFSTSTG 18
 Db 291 RSGRSGYSDRSGSISRFGTSNGR 313
 RESULT 29
 ID Q5KFX2 CRYNE PRELIMINARY; PRT; 699 AA.
 AC Q5KFX2;
 DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
 DT 15-FEB-2005, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Hypothetical protein.
 GN OrderedLocNames=CNF00280;
 OS Cryptococcus neoformans (Filobasidiella neoformans).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 OX NCBI_TaxID=5207;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=JRC21;
 RC PubMed=15653466; DOI=10.1126/science.1103773;
 RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
 RA Vanathavan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
 RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
 RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
 RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
 RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,
 RA Mathewson C.A., Mitchell T.G., Perteira R., Riggs P.R., Salzberg S.L.,
 RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
 RA Sun B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
 RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
 RA Fraser C.M., Hyman R.W.;
 RT "The genome of the basidiomycetous yeast and human pathogen
 RT Cryptococcus neoformans";
 RL Science 307:1321-1324 (2005).
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 CC -----
 CC EMBL; AB017346; AAW44148.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 699 AA; 75947 MW; 268A18BABE2B2A2 CRC64;
 Query Match 51.1%; Score 46.5; DB 2; Length 699;
 Best Local Similarity 52.2%; Pred. No. 62;
 Matches 12; Conservative 0; Mismatches 6; Indels 5; Gaps 1;
 QY 1 RGRGLYSRRRPFSTSTG 18
 Db 291 RSGRSGYSDRSGSISRFGTSNGR 313
 RESULT 30
 ID Q41486 GVIRU PRELIMINARY; PRT; 94 AA.
 AC Q41486;
 DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
 DT 01-JAN-1998, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE 11k protein.
 OS Potato virus S.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
 OC Carlavirus.
 OX NCBI_TaxID=12169;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=S-RB;
 RA Joung Y.H.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; U74376; AAB65087.1; -; Genomic RNA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_bd.
DR Pfam; PF01623; Carla_C4; 1.
SQ SEQUENCE 94 AA; 10650 MW; C8CCEFI0F00A10A CRC64;

Query Match 50.5%; Score 46; DB 2; Length 94;
Best Local Similarity 52.0%; Pred. No. 7.5;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CGRLSYSRFRSTGTG 18
Db 38 GGRSTYGRKRARSIGR 54

RESULT 31
ID Q3FAL7_9BURK PRELIMINARY; PRT; 233 AA.
AC Q3FAL7;
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DE Pirin, N-terminal.
DE Pirin, N-terminal.
GN ORFNames=BambDRAFT_2492;
OS Burkholderia ambifaria AMMD.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=339670;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AMMD;
RG US DOE Joint Genome Institute (JGI-PGP);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Burkholderia ambifaria
RT AMMD.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AMMD;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia ambifaria
RT AMMD.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAJL0100006; EAO45746.1; -; Genomic DNA.
DR InterPro; IPR012093; Pirin_N.
DR InterPro; IPR003829; Pirin_N.
DR Pfam; PF02678; Pirin; 1.
DR PIRSF; PIRSF06232; Pirin; 1.
SQ SEQUENCE 233 AA; 25062 MW; 183B8AA579CC51B6 CRC64;

Query Match 50.5%; Score 46; DB 2; Length 233;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGRGLSYSRFRSTGTG 18
Db 124 RGRPGVGAQRFRADDEKR 141

RESULT 32
ID O16689_CABEL PRELIMINARY; PRT; 236 AA.
O16689_CABEL
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AC O16689;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 2.
DT 07-FEB-2006, entry version 29.
DE Hypothetical protein.
GN ORFNames=K07E8.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
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CC -----
DR EMBL; AF016678; AAB66149.2; -; Genomic DNA.
DR PIR; T32047; T32047.
DR WormBase; WBGene00019495; K07E8.3.
DR WormPep; K07E8.3; CE29512.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR012340; OB_NA_bd_sub.
DR InterPro; IPR004365; OB_trNA_NA_bd.
DR Pfam; PF01336; tRNA_antl; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 236 AA; 26938 MW; 693B7ABB3795A6C9 CRC64;

Query Match 50.5%; Score 46; DB 2; Length 236;
Best Local Similarity 47.1%; Pred. No. 22;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGRGLSYSRFRSTGTG 17
Db 74 RGRVDYHDKRYPNRTG 90

RESULT 33
ID Q7PPF7_ANOGA PRELIMINARY; PRT; 288 AA.
AC Q7PPF7;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 2.
DT 07-FEB-2006, entry version 13.
DE ENSANGP0000022270 (Fragment).
GN ORFNames=ENSANG00000019781;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
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DR -----
DR EMBL; AA001008948; EAA10488.3; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signaln. .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Membrane; Receptor; Transducer;
KW Transmembrane.
FT NON TRR 1
SQ SEQUENCE 288 AA; 31036 MW; 39C256679D378FE7 CRC64;

Query Match 50.0%; Score 45.5; DB 2; Length 288;
Best Local Similarity 47.8%; Pred. No. 33;
Matches 11; Conservative 2; Mismatches 3; Indels 7; Gaps 1;

QY 3 GRLSYRRRPS-----TSGR 18
DB 131 GRLGFRRTFTCTVLPSTITGK 153

RESULT 34
HSPI_MACRU
ID HSPI_MACRU STANDARD; PRT; 59 AA.
AC P42142;
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Sperm protamine P1.
GN Name=PRM1;
OS Macropus rufus (Red kangaroo) (Megalala rufa).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9321;
RN [1]
RC TISSUE=Testis;
RP TISSUE=Testis;
RX MEDLINE=5215351; PubMed=7700877;
RA Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
RT "Molecular phylogeny and evolution of marsupial protamine P1 genes.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -1- SUBCELLULAR LOCATION: Nucleus.
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- SIMILARITY: Belongs to the protamine P1 family.
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DR EMBL; L35447; AAA74616.1; -; Genomic DNA.
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; Protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Developmental protein; Differentiation;
KW DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT_MET 0 0 By similarity.
FT CHAIN 1 59 Sperm protamine P1.
FT FTID=PRO_0000191494.
SQ SEQUENCE 59 AA; 8230 MW; 78F1AE592B4B2FA2 CRC64;

Query Match 49.5%; Score 45; DB 1; Length 59;
Best Local Similarity 69.2%; Pred. No. 5;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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DR -----
DR EMBL; AA001008948; EAA10488.3; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signaln. .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Membrane; Receptor; Transducer;
KW Transmembrane.
FT NON TRR 1
SQ SEQUENCE 288 AA; 31036 MW; 39C256679D378FE7 CRC64;

Query Match 50.0%; Score 45.5; DB 2; Length 288;
Best Local Similarity 47.8%; Pred. No. 33;
Matches 11; Conservative 2; Mismatches 3; Indels 7; Gaps 1;

QY 3 GRLSYRRRPS-----TSGR 18
DB 131 GRLGFRRTFTCTVLPSTITGK 153

RESULT 34
HSPI_MACRU
ID HSPI_MACRU STANDARD; PRT; 59 AA.
AC P42142;
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Sperm protamine P1.
GN Name=PRM1;
OS Macropus rufus (Red kangaroo) (Megalala rufa).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9321;
RN [1]
RC TISSUE=Testis;
RP TISSUE=Testis;
RX MEDLINE=5215351; PubMed=7700877;
RA Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
RT "Molecular phylogeny and evolution of marsupial protamine P1 genes.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -1- SUBCELLULAR LOCATION: Nucleus.
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- SIMILARITY: Belongs to the protamine P1 family.
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DR EMBL; L35447; AAA74616.1; -; Genomic DNA.
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; Protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Developmental protein; Differentiation;
KW DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT_MET 0 0 By similarity.
FT CHAIN 1 59 Sperm protamine P1.
FT FTID=PRO_0000191494.
SQ SEQUENCE 59 AA; 8230 MW; 78F1AE592B4B2FA2 CRC64;

Query Match 49.5%; Score 45; DB 1; Length 59;
Best Local Similarity 69.2%; Pred. No. 5;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 1 RGRRLSYRRRPS 13
DB 41 RGRRLSYRRRPS 53

RESULT 35
HSPI_CAEFU
ID HSPI_CAEFU STANDARD; PRT; 60 AA.
AC P42131;
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Sperm protamine P1.
GN Name=PRM1;
OS Caenolestes fuliginosus (Shrew opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Paucituberculata; Caenolestidae; Caenolestes.
OX NCBI_TaxID=37696;
RN [1]
RC NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP TISSUE=Sperm;
RX MEDLINE=5215351; PubMed=7700877;
RA Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
RT "Molecular phylogeny and evolution of marsupial protamine P1 genes.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -1- SUBCELLULAR LOCATION: Nucleus.
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- SIMILARITY: Belongs to the protamine P1 family.
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DR EMBL; L35332; AAA74598.1; -; Genomic DNA.
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; Protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Developmental protein; Differentiation;
KW DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT_MET 0 0 By similarity.
FT CHAIN 1 60 Sperm protamine P1.
FT FTID=PRO_0000191452.
SQ SEQUENCE 60 AA; 8514 MW; 7630E63AD33A9B05 CRC64;

Query Match 49.5%; Score 45; DB 1; Length 60;
Best Local Similarity 69.2%; Pred. No. 6.7;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RGRRLSYRRRPS 13
DB 41 RGRRLSYRRRPS 53

RESULT 36
HSPI_DASHA
ID HSPI_DASHA STANDARD; PRT; 60 AA.
AC P67834; P42133; P42135;
DT 11-OCT-2004, integrated into UniProtKB/Swiss-Prot.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Sperm protamine P1.
GN Name=PRM1;
OS Dasyurus hallucatus (Satanellus/northern quoll).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Dasyurus.
OX NCBI_TaxID=9280;
RN [1]
RC NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP TISSUE=Sperm;
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RX MEDLINE=95215351; PubMed=7700877;
RA Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
RT "Molecular phylogeny and evolution of marsupial protamine P1 genes.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
CC -!- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -!- SUBCELLULAR LOCATION: Nucleus.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- SIMILARITY: Belongs to the protamine P1 family.
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CC
CC -----
DR EMBL; L35341; AAA56795.1; -; Genomic_DNA.
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; Protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Developmental protein; Differentiation;
KW DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT_MET 0 0 By similarity.
FT CHAIN 1 60 Sperm protamine P1.
FT
FT
SQ SEQUENCE 60 AA; 8246 MW; 615D3D85E7123025 CRC64;
Query Match 49.5%; Score 45; DB 1; Length 60;
Best Local Similarity 69.2%; Pred. No. 6.7;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 RGRRLSYRRRFS 13
DB 42 RGRRGYSRRYS 54
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RESULT 37
HSP1 DENGQ
ID HSP1 DENGQ STANDARD; PRT; 60 AA.
AC P67838; Q9GQJ1;
DT 11-OCT-2004, integrated into UniProtKB/Swiss-Prot.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Sperm protamine P1.
GN Name=PRM1;
OS Dendrolagus goodfellowi (Goodfellow's tree kangaroo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Dendrolagus.
OX NCBI_TaxID=69260;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Burk A., Springer M.S.;
RT "Intergenic relationships among Macropodoidea (Metatheria:
RT Diprotodontia) and the chronicle of kangaroo evolution.";
RL J. Mammal. Evol. 7:213-237(2000).
CC -!- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -!- SUBCELLULAR LOCATION: Nucleus.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- SIMILARITY: Belongs to the protamine P1 family.
CC
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CC
CC -----
DR EMBL; AF187537; AAG27954.1; -; Genomic_DNA.
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; Protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Developmental protein; Differentiation;
KW DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT_MET 0 0 By similarity.
FT CHAIN 1 60 Sperm protamine P1.
FT
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SQ SEQUENCE 60 AA; 8246 MW; 615D3D85E7123025 CRC64;
Query Match 49.5%; Score 45; DB 1; Length 60;
Best Local Similarity 69.2%; Pred. No. 6.7;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 RGRRLSYRRRFS 13
DB 42 RGRRGYSRRYS 54
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RESULT 38
HSP1 MACPA
ID HSP1 MACPA STANDARD; PRT; 60 AA.
AC P42137;
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Sperm protamine P1.
GN Name=PRM1;
OS Macropus agilis (Agile wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9313;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC TISSUE=Sperm;
RX MEDLINE=95215351; PubMed=7700877;
RA Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
RT "Molecular phylogeny and evolution of marsupial protamine P1 genes.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
CC -!- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -!- SUBCELLULAR LOCATION: Nucleus.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- SIMILARITY: Belongs to the protamine P1 family.
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CC
CC -----
DR EMBL; L35451; AAA74615.1; -; Genomic_DNA.
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; Protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Developmental protein; Differentiation;
KW DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT_MET 0 0 By similarity.
FT CHAIN 1 60 Sperm protamine P1.
FT
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SQ SEQUENCE 60 AA; 8339 MW; 96255C818921EB85 CRC64;
Query Match 49.5%; Score 45; DB 1; Length 60;
Best Local Similarity 69.2%; Pred. No. 6.7;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 RGRRLSYRRRFS 13
DB 41 RGRRGYSRRYS 53
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RESULT 39
HSP1 MACPA
ID HSP1 MACPA STANDARD; PRT; 60 AA.
AC Q9GLQ9;
DT 16-NOV-2001, integrated into UniProtKB/Swiss-Prot.
DT 16-NOV-2001, sequence version 2.
DT 07-FEB-2006, entry version 23.
DE Sperm protamine P1.
GN Name=PRM1;
OS Macropus parryi (Whiptail wallaby).
FT
FT
SQ SEQUENCE 60 AA; 8339 MW; 96255C818921EB85 CRC64;
Query Match 49.5%; Score 45; DB 1; Length 60;
Best Local Similarity 69.2%; Pred. No. 6.7;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 RGRRLSYRRRFS 13
DB 41 RGRRGYSRRYS 53
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9318;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Burk A., Springer M.S.;
RT "Intergenic relationships among Macropodoidea (Metatheria;
RT Diprotodontia) and the chronicle of kangaroo evolution.";
RL J. Mammal. Evol. 7:213-237(2000).
CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -1- SUBCELLULAR LOCATION: Nucleus.
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- SIMILARITY: Belongs to the protamine P1 family.
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CC

DR EMBL; AF187533; AAC27950.1; -; Genomic_DNA.
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; Protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE P1; 1.
KW Chromosomal protein; Developmental protein; Differentiation;
KW DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT MET 0 0 By similarity.
FT CHAIN 1 60 Sperm protamine P1.
SQ SEQUENCE 60 AA; 8370 MW; C68F5C81892B4B22 CRC64;
Query Match 49.5%; Score 45; DB 1; Length 60;
Best Local Similarity 69.2%; Pred. No. 6.7;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RGRRLSYRRRFS 13
Db 41 RGRRRGYRRRYS 53
RESULT 40
HSP1_ONCFR STANDARD; PRT; 60 AA.
AC Q9GLQ3;
DT 16-NOV-2001, integrated into UniprotKB/Swiss-Prot.
DT 16-NOV-2001, sequence version 2.
DE 07-FEB-2006, entry version 23.
DE Sperm protamine P1.
GN Name=PRM1;
OS Onychogalea fraenata (Bridled nail-tailed wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Onychogalea.
OX NCBI_TaxID=114227;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Burk A., Springer M.S.;
RT "Intergenic relationships among Macropodoidea (Metatheria;
RT Diprotodontia) and the chronicle of kangaroo evolution.";
RL J. Mammal. Evol. 7:213-237(2000).
CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -1- SUBCELLULAR LOCATION: Nucleus.
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- SIMILARITY: Belongs to the protamine P1 family.
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CC

DR EMBL; AF187542; AAC27959.1; -; Genomic_DNA.
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; Protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE P1; 1.

KW Chromosomal protein; Developmental protein; Differentiation;
KW DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT MET 0 0 By similarity.
FT CHAIN 1 60 Sperm protamine P1.
SQ SEQUENCE 60 AA; 8325 MW; AD48EFC92BA94B27 CRC64;
Query Match 49.5%; Score 45; DB 1; Length 60;
Best Local Similarity 69.2%; Pred. No. 6.7;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RGRRLSYRRRFS 13
Db 41 RGRRRGYRRRYS 53

Search completed: May 21, 2006, 00:24:02
Job time : 296 secs

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